

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2004, 14:17:16 ; Search time 303 Seconds  
(without alignments)  
9197.419 Million cell updates/sec

Title: US-10-060-066-2

Perfect score: 656  
Sequence: 1 tatggtctactctgacct.....tgctattctattctcttg 656

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

N\_Geneseq\_29Jan04:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001s:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002s:\*  
7: geneseqn2003as:\*  
8: geneseqn2003bs:\*  
9: geneseqn2003cs:\*  
10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96.4	14.7	1173	7 ABX72170	Abx72170 Human NOV
2	86.4	13.2	984	3 AA299791	Aa299791 DNA encod
3	86.4	13.2	984	4 AAF81301	Aaf81301 Human cac
4	83.2	12.7	1071	6 ABK51915	Abk51915 DNA enco
5	73.2	11.2	1093	6 ABQ17109	Abq17109 Oligonuc
6	73.2	11.2	1093	6 ABQ17108	Abq17108 Oligonuc
7	54.4	8.3	972	3 AA299795	Aa299795 DNA encod
8	54.4	8.3	1252	4 ABA09049	Abao9049 Human vol
9	54.4	8.3	1478	3 AA251628	Abk51628 Human mem
10	53.6	8.2	1477	6 ABK51914	Abk51914 DNA enco
11	52.8	8.0	1558	6 ABK51913	Abk51913 DNA enco
12	52	7.9	945	3 AA299794	Aa299794 EST corre
13	52	7.9	948	3 AA299793	Aa299793 DNA encod
14	52	7.9	1383	4 ABA09004	Abao9004 Human vol
15	52	7.9	1854	3 AAC77216	Abv77216 Human ORF
16	52	7.9	3914	6 ABV76746	Abv76746 Human ple
17	45.8	7.0	110000	4 AA199682_16	Continuation (17 o
18	45.8	7.0	110000	4 AA199683_16	Continuation (17 o
19	43.6	6.6	451	9 ABT10409	Abt10409 Human bre
20	43	6.6	1031	9 AAD29576	Aad29576 Human tum
21	42.8	6.5	799	2 AA55831	Aa55831 Nucleotid
22	42.8	6.5	1925	2 AA30924	Aax90924 Epstein B
23	42.8	6.5	1926	3 AA50254	Aaa50254 Epstein B

C 24	42.8	6.5	1926	4 AAF82902	Aaf82902 EBV tethe
C 25	42.8	6.5	2580	3 AA75454	Aa75454 Nucleotid
C 26	42.8	6.5	2580	6 AA164275	Aa164275 Epstein-B
C 27	42.8	6.5	5452	2 AAX90923	Aax90923 Anti-gens
C 28	42.8	6.5	8705	2 AA23778	Aa23778 Vector PS
C 29	42.8	6.5	9600	2 AA21683	Aa21683 Vector pl
C 30	42.8	6.5	10285	6 AB871027	Ab871027 pCEP-Xa-P
C 31	42.8	6.5	10285	6 AB866453	Ab866453 Plasmid p
C 32	42.8	6.5	10386	2 AA222248	Aa222248 Nucleotid
C 33	42.8	6.5	10596	2 AA051721	Aa051721 Plasmid p
C 34	42.8	6.5	10596	2 AA15650	Aa15650 Nucleotid
C 35	42.8	6.5	10596	2 AA140348	Aa140348 Plasmid p
C 36	42.8	6.5	16080	3 AA59553	Aa59553 DNA clone
C 37	42.6	6.5	585	6 AB050506	Ab050506 Oligonuc
C 38	42.6	6.5	585	6 AB050507	Ab050507 Oligonuc
C 39	42.4	6.5	1000	3 AAA02484	Aaa02484 Human col
C 40	42.4	6.5	8837	9 ADD25495	Add25495 Binding d
C 41	42.2	6.4	615	7 ACA23975	Aca23975 Prokaryot
C 42	41.8	6.4	415	4 AA182119	Aa182119 Human pol
C 43	41.6	6.3	541	3 AAC07568	Aac07568 Human sec
C 44	41.6	6.3	1646	3 AA235999	Aa235999 S. klara
C 45	41.4	6.3	12733	6 ABK98631	Abk98631 Vector ps

## ALIGNMENTS

RESULT 1	ABX72170	standard; cDNA; 1173 BP.
ID	ABX72170	
XX	XX	
AC	ABX72170;	
XX	XX	
DT	03-JUN-2003	(first entry)
XX	XX	
DE	Human NOVX polynucleotide #1.	
XX	XX	
KW	Human; NOVX; gene; ser; metabolic disorder; cardiomyopathy; diabetes; ASD;	
KW	hypertension; congenital heart defect; aortic stenosis; valve disease;	
KW	atrial septal defect; atrioventricular canal defect; ductus arteriosus;	
KW	pulmonary stenosis; subaortic stenosis; ventricular septal defect; VSD;	
KW	tuberous sclerosis; scleroderma; atherosclerosis; infectious disease;	
KW	obesity; anorexia; neurodegenerative disorder; Alzheimer's disease;	
KW	Parkinson's disease; immune disorder; haematopoietic disorder;	
KW	haemophilia; hypercoagulation; Crohn's disease; cancer.	
OS	Homo sapiens.	
XX	XX	
PN	WO200281498-A2.	
XX	XX	
PD	17-OCT-2002.	
XX	XX	
PF	03-APR-2002; 2002WO-US010780.	
XX	XX	
PR	03-APR-2001; 2001US-0281086P.	
PR	03-APR-2001; 2001US-0281136P.	
PR	05-APR-2001; 2001US-0281863P.	
PR	05-APR-2001; 2001US-0281906P.	
PR	06-APR-2001; 2001US-0282020P.	
PR	10-APR-2001; 2001US-0282930P.	
PR	10-APR-2001; 2001US-0282934P.	
PR	12-APR-2001; 2001US-0283512P.	
PR	13-APR-2001; 2001US-0283710P.	
PR	17-APR-2001; 2001US-0284234P.	
PR	19-APR-2001; 2001US-0285325P.	
PR	20-APR-2001; 2001US-0285381P.	
PR	20-APR-2001; 2001US-0285609P.	
PR	23-APR-2001; 2001US-0285748P.	
PR	23-APR-2001; 2001US-0285890P.	
PR	24-APR-2001; 2001US-0286088P.	
PR	25-APR-2001; 2001US-0286292P.	
PR	27-APR-2001; 2001US-0287213P.	
PR	02-MAY-2001; 2001US-0288257P.	

PR 29-MAY-2001; 2001US-0294164P.  
 PR 30-MAY-2001; 2001US-0294484P.  
 PR 18-JUN-2001; 2001US-0298952P.  
 PR 19-JUN-2001; 2001US-0299237P.  
 PR 19-JUN-2001; 2001US-0299276P.  
 PR 12-SEP-2001; 2001US-0318750P.  
 PR 25-SEP-2001; 2001US-0324802P.  
 PR 25-SEP-2001; 2001US-0324802P.  
 PR 27-SEP-2001; 2001US-0325684P.  
 PR 17-OCT-2001; 2001US-0330143P.  
 PR 14-NOV-2001; 2001US-0332131P.  
 PR 14-NOV-2001; 2001US-0332240P.  
 PR 14-NOV-2001; 2001US-0332779P.  
 PR 21-NOV-2001; 2001US-0332115P.  
 PR 04-DEC-2001; 2001US-0337621P.  
 PR 03-JAN-2002; 2002US-0345783P.  
 PR 16-JAN-2002; 2002US-0350251P.  
 PR 02-APR-2002; 2002US-00114270.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Guo X, Kekuda R, Miller CE, Malyankar UM, Spytek KA;  
 PI Paturnajan M, Liu X, Gusev VY, Li L, Vernet CAM, Zernhusen BD;  
 PI Gorman L, Shenoy SG, Pena CE, Smithson G, Burgess CE, Gerlach V;  
 PI Padigaru M, Shimketa RA, Gangoli EA, Taupier RJ, Casman SJ, Ji W;  
 PI Anderson DM, Leite MW, Raetelli L, Edinger SR, Stone DJ;  
 PI MacDougall JR, Rothenberg ME, Mazur A, Miller I, Peyman JA;  
 PI Ellerman K;  
 DR WPI: 2003-046858/04.  
 DR P-PSDB; ABUS4542.  
 XX

PT New isolated NOVX polypeptide useful for treating atherosclerosis,  
 PT metabolic disorders, diabetes, obesity, infectious disease, anorexia,  
 PT neurodegenerative disorders, Alzheimer's disease and cancer.  
 XX  
 PS Claim 17; Page 91; 666pp; English.  
 XX

CC The invention relates to human polypeptides, termed NOVX, and the  
 CC polynucleotides encoding them. The polypeptides and polynucleotides are  
 CC useful for diagnosing disease, and screening for potential therapeutic  
 CC agents. The sequences are useful for treating metabolic disorders,  
 CC cardiomyopathy, diabetes, hypertension, congenital heart defects, aortic  
 CC stenosis, atrial septal defect (ASD), atrioventricular canal defect,  
 CC ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular  
 CC septal defect (VSD), valve diseases, tuberos sclerosis, scleroderma,  
 CC atherosclerosis, obesity, infectious disease, anorexia, neurodegenerative  
 CC disorders, Alzheimer's disease, Parkinson's disease, immune disorders,  
 CC haematopoietic disorders, haemophilia, hypercoagulation, Crohn's disease  
 CC and cancer. Sequences ABX72170-ABX72275 represent human NOVX  
 CC polynucleotides of the invention  
 XX

XX Sequence 1173 BP; 246 A; 386 C; 347 G; 194 T; 0 U; 0 Other;

Query Match 14.7%; Score 96.4; DB 7; Length 1173;  
 Best Local Similarity 83.8%; Pred. No. 3.8e-15;  
 Matches 109; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 187 TGAACGCTGGAATGAAGAGAGGGGTTTGTTGTTGAAAGGCGCTTACGTAATCACTCA 246  
 DB 38 TGAAGGCTGGAACGAATGCGGGGCTTGTGTGAGAGAGGGGTGAGGGTGTGCTGA 97  
 QY 247 CCACCATCGGCGCCTTCCGCGCTTTTGCGCTCATGACCATCGCATTCAGCACTGACTACT 306  
 DB 98 CGACGCTGGCGCCTTCCGCGCCTTCCGCGCTCATGACCATCGCATTCAGCACTGACTACT 157  
 QY 307 GCGTCTACAC 316  
 DB 158 GCGTCTACAC 167

RESULT 2  
 AAZ9791

ID AAZ9791 standard; DNA; 984 BP.  
 XX  
 AC AAZ9791;  
 XX  
 DT 12-JUL-2000 (first entry)  
 XX  
 DE DNA encoding a voltage-gated calcium channel designated CACNGLIKE3.  
 XX  
 XX Human; skeletal muscle; voltage-gated calcium channel; CACNGLIKE3;  
 XX neurological disorder; epilepsy; stroke; head trauma; migraine;  
 XX affective disorder; depression; anxiety; schizophrenia; pain; cancer;  
 XX neurodegenerative disorder; Alzheimer's disease; cognitive disorder;  
 XX chromosome localisation; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..984  
 FT /tag= A  
 FT /product= "voltage-gated calcium channel"

XX MO200014224-A1.  
 XX  
 XX 16-MAR-2000.  
 XX  
 XX 06-SEP-1999; 99WO-GB002944.  
 XX  
 XX 08-SEP-1998; 98GB-00019592.  
 XX  
 XX (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX  
 XX Duckworth DM, Hayes PD;  
 XX  
 XX WPI: 2000-256976/22.  
 XX  
 XX P-PSDB; AAY84372.  
 DR

PT Isolated voltage-gated calcium channel polypeptide, designated  
 PT CACNGLIKE3, to treat diseases such as neurological disorders, epilepsy,  
 PT neurodegenerative disorders, cognitive disorders and cancer; comprises  
 PT 327 amino acid sequence.  
 XX  
 XX Claim 4; Page 31; 37pp; English.  
 XX

CC The present sequence encodes a human skeletal muscle voltage-gated  
 CC calcium channel polypeptide, designated CACNGLIKE3. The CACNGLIKE3  
 CC polypeptide and polynucleotide are useful in the treatment of diseases  
 CC such as neurological disorders, epilepsy, stroke, head trauma, migraine,  
 CC affective disorders including depression and anxiety, schizophrenia,  
 CC neurodegenerative disorders including Alzheimer's disease, cognitive  
 CC disorders, types of pain and cancer. The polynucleotide is also valuable  
 CC for chromosome localisation studies. The CACNGLIKE3 polypeptide and  
 CC polynucleotide are also useful in diagnostic assays for detecting  
 CC diseases associated with inappropriate CACNGLIKE3 activity or levels  
 XX  
 XX Sequence 984 BP; 206 A; 319 C; 265 G; 194 T; 0 U; 0 Other;

Query Match 13.2%; Score 86.4; DB 3; Length 984;  
 Best Local Similarity 66.8%; Pred. No. 1.5e-12;  
 Matches 123; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 214 TGTGTGTGAAAAGGGGCTTACGTAATCACTGACCAACGCGGCTTCCGCGCTTTTG 273  
 DB 5 TGCATGTGACCGGGGGCTGAGATGCTGTGACACAGCGCGGAGCTTCCCGCTTCT 64  
 QY 274 GCTTCATGACCATGGCCATGACGCTGACTACTGTGGCTTACACAGAGCTTCACTTCA 333  
 DB 65 GCTTCATGCGCCATGCGCATGCGACGACCTAATGCTGTACTTCAAGCGCGGACATCTGCA 124  
 QY 334 ACACCAACCACTCAGACAGAGGTATGACGACCAACCCCATCTGTGGGGGAGTGGCTCT 393  
 DB 125 ACGGACCAACCTAATCACTGACGACGAGCGGGGGGGGGGGGGGGGGGGGCACTCA 184  
 QY 394 CCGA 397

Db 185 CCCA 188

RESULT 3  
ID AAF81301 standard; cDNA; 984 BP.  
XX AAF81301;  
AC AAF81301;  
XX 01-JUN-2001 (first entry)  
XX Human cacng8 cDNA.  
XX Human: atargazin-like; CACNG8; anticonvulsant; hypotensive; vasotropic;  
XX antirhythmic; antitremor; analgesic; nootropic; cytosolic;  
XX neuroprotective; cerebroprotective; antidiabetic; antiallergic;  
XX antileptocytic; immunosuppressive; antiparkinsonian; auditory;  
XX ophthalmological; tranquilizer; neuronal disorder;  
XX calcium channel modulation; ss.  
XX Homo sapiens.  
XX WO200121791-A2.  
XX 29-MAR-2001.  
XX 25-SEP-2000; 2000MO-GB003685.  
XX 23-SEP-1999; 99GB-00022571.  
XX (GLAXO) GLAXO GROUP LTD.  
XX Clare JJ, Plumpton M, Mose FJ, Saneau P;  
XX MPI; 2001-266074/27.  
XX P-PSDB; AAB73979.  
XX Novel atargazin-like polypeptides capable of modulating the steady state  
XX inactivation of an alpha pore-forming subunit of a voltage-gated calcium  
XX channel, for treating central nervous system disorders.  
XX  
XX Claim 6; Page 38-39; 48pp; English.  
XX  
XX The present sequence is provided in a specification relating to an  
XX isolated atargazin-like polypeptide comprising a sequence of 327 or 275  
XX amino acids fully defined in the specification, or its variant capable of  
XX modulating the steady state. The polypeptide is useful for treating a  
XX subject having a neuronal disorder that is responsive to calcium channel  
XX modulation. It is useful in the manufacture of a medicament for treatment  
XX or prophylaxis of a disorder that is responsive to calcium channel  
XX modulation, e.g. epilepsy, episodic ataxia, spinocerebellar ataxia,  
XX hypertension, ischaemic heart disease, arrhythmia, angina, pain, cerebral  
XX ischaemia, Alzheimer's disease, neuroprotection, stroke, diabetes,  
XX cerebral vasospasm, atherosclerosis, cardiac dysrhythmias, peripheral  
XX vascular disease, immunosuppression, cancerous diseases, migraine,  
XX headache, bipolar disorder, unipolar depression, anxiety, Parkinson's  
XX disease, cognitive disorders, ophthalmic diseases, neuromuscular  
XX disorders and tinnitus. Nucleic acids encoding these polypeptides are  
XX useful in the production of the polypeptides, and as primers  
XX  
XX Sequence 984 BP; 204 A; 319 C; 265 G; 194 T; 0 U; 2 Other;  
XX  
XX Query Match 13.2%; Score 86.4; DB 4; Length 984;  
XX Best Local Similarity 66.8%; Pred. No. 1.5e-12;  
XX Matches 123; Conservative 0; Mismatches 61; Indels 0; Gaps 0;  
XX  
XX 214 TGTGCTGTAAGGCGCTCAGTACTCTGTCACCACTGCGCGCTTGGCGCTTTG 273  
XX 5 TGGATGCGACCGCGGCTGCAATGCTGACCAAGCGCGGAGCTTGGCGCTTCT 64  
XX 274 GCGTCATGACCATGCGCATGACATGACTGCTTACACAAAGAGCTTCATCTGCA 333

Db 65 CCTCATGCGCATCGCCATCGGCACCGACTAGCTGTACTCCAGCGGCACATCTGCA 124  
QY 334 ACACGACCAACCTCAGAGATGATGACGACACCCCATGTGGGGGACATGGCTCT 393  
Db 125 ACGGACCAACTGACATGACAGAGGCGCCCGCCCGCGCGCGGAGACTCA 184  
QY 394 CCGA 397  
Db 185 CCCA 188

RESULT 4  
ID AAK51915 standard; cDNA; 1071 BP.  
XX AAK51915;  
AC AAK51915;  
XX 13-AUG-2002 (first entry)  
XX cDNA encoding mouse Cacng4.  
XX Mouse; neuronal voltage-gated calcium channel gamma subunit;  
XX autoimmune disease; Lambert-Baton syndrome; neuronal disease; epilepsy;  
XX immunosuppressive; anticonvulsant; Cacng4; gene; ss.  
XX Murinae gen. sp.  
XX  
XX Key Location/Qualifiers  
XX 5'UTR 1..21  
XX /tag= a  
XX CDS 22..1005  
XX /tag= b  
XX /product= "Cacng4 #1"  
XX 22..1005  
XX /tag= c  
XX /product= "Cacng4 #2"  
XX /transl\_except= (pos:979..981, aa:Xaa)  
XX /transl\_except= (pos:991..993, aa:Xaa)  
XX /note= "Xaa= unknown"  
XX 1006..1071  
XX /tag= d  
XX  
XX US6365337-B1.  
XX  
XX 02-APR-2002.  
XX 27-JUL-1998; 98US-00123030.  
XX 27-JUL-1998; 98US-00123030.  
XX (IOWA) UNIV IOWA RES FOUND.  
XX (JACK-) JACKSON LAB.  
XX Letts VA, Frankel WN, Campbell KP, Felix R, Biddlecome G;  
XX MPI: 2002-433421/46.  
XX P-PSDB; AAU97155, AAU97156.  
XX  
XX Novel nucleic acid sequences encoding a neuronal voltage-gated calcium  
XX channel gamma subunit useful in screening for compounds which modulate  
XX activity of the channel and in diagnosing, treating neuronal diseases.  
XX  
XX Disclosure; Fig 7; 36pp; English.  
XX  
XX The present invention relates to the isolation of mouse genes encoding  
XX neuronal voltage-gated calcium channel gamma subunits designated Cacng2,  
XX Cacng3, and Cacng4. The genes are useful for identifying candidate  
XX compounds for modulating the activity of human neuronal voltage-gated  
XX calcium channels. They are also useful for diagnosing and treating the  
XX autoimmune disease Lambert-Baton syndrome, as well as diagnosing defects  
XX in gamma subunit genes of a patient with a neuronal disease such as  
XX epilepsy. The present sequence encodes mouse Cacng4. Note: Nucleotides 1-  
XX 21 of the present sequence are not shown in Fig 7 but are included in the

CC	sequence shown in the sequence listing	
XX	Sequence 1071 BP, 227 A; 345 C; 284 G; 213 T; 0 U; 2 Other;	
50	Query Match 12.7%; Score 83.2; DB 6; Length 1071; Best Local Similarity 65.8%; Pred. No. 1.1e-11; Matches 121; Conservative 0; Mismatches 63; Indels 0; Gaps 0	
Oy	214 TGTGGTGTGAAAAGGCGCTTCAAGTACTATACACCAATCGAGCGCTTGTG	273
Db	26 TGCATGTGGACCGCGGGCTGCAAGATGCTCTACACAGGCGGAGCCCTTGGCCCTTCT	85
Oy	274 GCCTCATACCAATCGCCATCAGCACTGACTACTGGCTTACAAAGCTTCATCTGCA	333
Db	86 CGCTCATGGCCATCCGCCATCGGCACCGAATACCGGCTGTACTCCAGCGGCATCTGCA	145
Oy	334 ACACCAACAACCTTCACAGAGGTGATGACGACCAACCCATGTTGGGGCAATGGCTCT	393
Db	146 ACGGACACCAACTGACATGACGACGAGGCCCCCGCCGCCGCTCGCGGAGCACTCA	205
Oy	394 CCGA 397	
Db	206 CCGA 209	

CC	(i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC	and of a wide range of diseases, e.g. cancer, disorders of the central
CC	nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC	particularly by detecting mutations or single nucleotide polymorphisms
CC	(SNP's); and (ii) for differentiation of cell or tissue types and for
CC	investigating cell differentiation. The method allows the methylation
CC	status of many C residues to be determined simultaneously. SEQID310-
CC	AB054191 represent genomic DNA sequences used to illustrate the method
CC	for determining the degree of cytosine methylation described in the
CC	disclosure of the invention
XX	
SQ	Sequence 1093 BP; 439 A; 406 C; 153 G; 95 T; 0 U; 0 Other;
Query Match	11.2%; Score 73.2; DB 6; Length 1093;
Best Local Similarity	65.1%; Pred. No. 4.4e-09;
Matches 108; Conservative	0; Mismatches 58; Indels 0; Gaps 0
DG	232 TTCAAGTACTACTGCACCAACCATCGGGCGCTTCGGCGGCTTTTGAGCCTCATGACCATTGCCA 291 
DG	411 TACAATAACTACTATACCAAGAACCGAACTTGGCGCGCTTTCGGCTCATTAACCATGCGCCA 470 
DY	232 TCAGCACTGACTACTGGGCTTACACAGAAGCTCTATCTTGCAACACACCAACCTCACAG 351 
DG	471 TCGAACACGCACTACTTAATCTACTCCAAACGCGCACATCTACACAGACACCAACTTACCA 530 
DY	352 CAGGTGATGACGAGCAACCAACCCCATCTGTGGGGGAGTAGTGCTCTTCGCA 397 
DG	531 TAACAGACGAACCCCCCGCCCGCCGCGCCGCGCGAGACCTTACCA 576 

CC The amplicon is hybridised to two classes, each with at least one member,  
 CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the  
 CC degree of hybridisation to both classes is determined from the label on  
 CC the amplicon. From the ratio of labels hybridised to the two classes of  
 CC oligomers, the degree of methylation is calculated. The method is used:  
 CC (1) for diagnosis and/or prognosis of side effects of therapeutic drugs  
 CC and of a wide range of diseases, e.g. cancer, disorders of the central  
 CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,  
 CC particularly by detecting mutations or single nucleotide polymorphisms  
 CC (SNP's) and (ii) for differentiation of cell or tissue types and for  
 CC investigating cell differentiation. The method allows the methylation  
 CC status of many C residues to be determined simultaneously. ABQ13410-  
 CC ABQ5121 represent genomic DNA sequences used to illustrate the method  
 CC for determining the degree of cytosine methylation described in the  
 CC disclosure of the invention

XX Sequence 1093 BP; 95 A; 153 C; 406 G; 439 T; 0 U; 0 Other;

Query Match 11.2%; Score 73.2; DB 6; Length 1093;

Best Local Similarity 65.1%; Pred. No. 4.4e-09;

Matches 108; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

DB 232 TTCAGTACTACTGACCAACCGGCGCTTGGCTTCATGACCATGCGCA 291

DB 683 TACAAATCTACTTAAACGACGACCGAAACCTTCCGCTTCATTAACCATGCGCA 624

QY 292 TCAGCAGTACTACTGCTCTACAGAGCTCTCATTCGCAACACCAACCTCAGAG 351

DB 623 TCGACACCGCATCTACTACTATCTCAACGCGCAGCATCTCAACGACCAACCTAACCA 564

QY 352 CAGGTGATGACGAGCCACCCCATCTGCGGCGCAGTGGCTCTCCGA 397

DB 563 TAAACGACGACACCCCGCCGCGCGCCGCGACGACCTCAGCA 518

RESULT 7

AA29795

ID AA29795 standard; DNA; 972 BP.

XX AA29795;

DT 12-JUL-2000 (first entry)

DE DNA encoding a voltage-gated calcium channel designated CACNG1K1.

KW Human; voltage-gated calcium channel; CACNG1K1; neurological disorder;

KW epilepsy; stroke; head trauma; migraine; affective disorder; depression;

KW anxiety; schizophrenia; neurodegenerative disorder; Alzheimer's disease;

KW cognitive disorder; pain; cancer; chromosome localization; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

XX CDS 1..972

XX FT /product= "voltage-gated calcium channel"

XX PN WO200014223-A1.

XX PD 16-MAR-2000.

XX PF 06-SEP-1999; 99WO-GB002937.

XX PR 07-SEP-1998; 98GB-00019474.

XX PA (SMK) SMITHKLINE BEECHAM PLC.

XX PI Duckworth DM, Hayes PD;

XX DR WPI; 2000-256975/22.

XX P-PSDB; AAI84376.

PT New human voltage-gated calcium channel, known as CACNG1K1, useful in

PT the treatment of diseases such as neurological disorders, epilepsy,  
 PT neurodegenerative disorders, cognitive disorders and cancer, comprises a  
 PT 323 amino acid sequence.

XX Claim 4; Page 30; 35pp; English.

XX The present sequence encodes a human voltage-gated calcium channel, known  
 CC as CACNG1K1. The CACNG1K1 polypeptide and polynucleotide are useful  
 CC in the treatment of diseases such as neurological disorders, epilepsy,  
 CC stroke, head trauma, migraine, affective disorders including depression  
 CC and anxiety, schizophrenia, neurodegenerative disorders including  
 CC Alzheimer's disease, cognitive disorders, types of pain and cancer. The  
 CC polynucleotide is also valuable for chromosome localization studies.  
 CC CACNG1K1 polypeptide and polynucleotide are also useful in diagnostic  
 CC assays for detecting diseases associated with inappropriate CACNG1K1  
 CC activity or levels

XX Sequence 972 BP; 231 A; 311 C; 231 G; 199 T; 0 U; 0 Other;

Query Match 8.3%; Score 54.4; DB 3; Length 972;

Best Local Similarity 70.2%; Pred. No. 0.00036;

Matches 73; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 218 GTGTGAAAAGGCGTTACAGTACTGACACCATCGGCGCTTGGCGCTTTGGCCT 277

DB 9 GTTATGAGGAGTTTCAATGCTTTTAAACACCGTGGCTTGGCTTGGCTTACGCT 68

QY 278 CATGACATCGGCATGACGATGACTACTGCTCTTACAGAG 321

DB 69 GATGACATATGCTGTGGAAACGACATATGCTTACTTCAAG 112

RESULT 8

ABA09049

ID ABA09049 standard; cDNA; 1252 BP.

XX ABA09049;

DT 11-JAN-2002 (first entry)

DE Human voltage gated Ca channel subunit homologue cDNA, SEQ ID NO:825.

KW Human; cytokine; cell proliferation; tissue growth; immunomodulator; activin;

KW inhibin; chemotaxis; chemokinesis; cancer; tumour; haematopoietic disorder;

KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;

KW chronic inflammatory condition; proliferative retinopathy;

KW atherosclerosis; coronary heart disease; arterial ischaemia;

KW bone disorder; osteoporosis; vascular growth disorder;

KW tissue regeneration; wound healing; infection; immune disorder;

KW cell culture; drug screening; gene therapy; antiinflammatory;

KW antiaesthetic; antiarthritic; haemostatic; antiarteriosclerotic;

KW cytosolic; osteopathic; vasotropic; cardiac; virucide; antibacterial;

KW antifungal; vulnery; antitumor; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

XX CDS 1..972

XX FT /product= "voltage-gated calcium channel"

XX PN WO200157188-A2.

XX PD 09-AUG-2001.

XX PF 05-FEB-2001; 2001WO-US003800.

XX PR 03-FEB-2000; 2000US-00496914.

XX PR 27-APR-2000; 2000US-00560875.

XX PA (HSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Drmanac RT;

XX DR WPI; 2001-457740/49.

XX P-PSDB; ABB11805.

XX Human proteins and DNA encoding sequences useful for preventing, treating  
PT or ameliorating a medical condition in a mammalian subject e.g. arthritis  
PT and cancer.  
XX  
XX Claim 1; Page 731-732; 1963pp; English.  
XX  
XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and  
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The  
CC invention also relates to vectors and recombinant host cells comprising a  
CC nucleotide of the invention, methods of producing the novel polypeptides,  
CC antibodies against the polypeptides, methods of detecting the nucleotides  
CC or polypeptides in a sample, and methods of identifying compounds which  
CC bind to polypeptides of the invention. Although novel, many of the  
CC polypeptides of the invention have homology to known proteins, thereby  
CC giving an insight into their probable biological activities, and hence  
CC potential therapeutic applications. The polypeptides of the invention may  
CC have various activities, including cytokine, cell proliferation or cell  
CC differentiation activities; stem cell growth factor activity;  
CC haematopoiesis regulatory activity; tissue growth activity;  
CC immunomodulatory activity; activin- or inhibin-related activities;  
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or  
CC thrombolytic activities; receptor or ligand activities; or may be  
CC involved in oncogenesis, cancer cell proliferation or metastasis.  
CC Depending on their biological activities, polypeptides and nucleotides of  
CC the invention are useful for preventing, treating or ameliorating medical  
CC conditions, e.g., by protein or gene therapy. Such conditions include  
CC cancers, haematopoietic disorders (e.g. myeloid or lymphoid cell  
CC disorders), chronic inflammatory conditions (e.g. asthma or arthritis),  
CC proliferative retinopathy, atherosclerosis, coronary heart disease,  
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal  
CC vascular growth. Polypeptides involved with tissue regeneration and  
CC repair (or nucleic acids encoding them) may be used to promote wound  
CC healing (e.g., of burns, incisions and ulcers), while those with  
CC immunomodulatory activities may be used in the treatment of viral,  
CC bacterial and fungal infections in addition to immune disorders.  
CC Polypeptides with growth factor activity may be used in cell cultures to  
CC promote cell growth. For example, such polypeptides may be used to  
CC manipulate stem cells in culture to give rise to neuroepithelial cells  
CC that can be used to augment or replace cells damaged by illness.  
CC autoimmune diseases or accidental damage. The polypeptides and nucleotides  
CC may also be used in the diagnosis of the above conditions, and in drug  
CC screening techniques. The present sequence represents a cDNA encoding a  
CC novel human polypeptide of the invention  
XX  
XX  
SQ Sequence 1252 BP; 302 A; 371 C; 266 G; 313 T; 0 U; 0 Other;  
Query Match 8.3%; Score 54.4; DB 4; Length 1252;  
Best Local Similarity 70.2%; Pred. No. 0.00039;  
Matches 73; Conservative 0; Mismatches 31; Indels 0; Gaps 0;  
OY 218 GTGTGAAAAGGCGCTTCACTGACACCATCGGCGCTTGGGCT 277  
DB 231 GTTTATGAGAGGTTCCTCAATCTTTTAAACACCGTTGGTCTTGCGCTTCAAGCT 350  
OY 278 CATGACCATCGGCATCAGCATGACTACTGCTCTTACACAGAG 321  
DB 351 GATGACCATAGCTGTGGGAAACGACATATGCTTCACTCAAG 394  
RESULT 9  
AAZ51628  
AAZ51628 standard; cDNA; 1478 BP.  
XX  
XX AAZ51628;  
XX  
XX 21-JUN-2000 (first entry)  
XX  
XX Human membrane channel protein-12 (MECHP-12) cDNA.  
XX  
XX Membrane channel protein-12; MECHP-12; diagnosis; treatment; lymphoma;  
XX cell proliferative disorder; bursitis; atherosclerosis; cancer; sarcoma;  
XX inflammatory disorder; AIDS; Addison's disease; cystic fibrosis; asthma;  
XX

KW diabetes mellitus; osmoregulatory disorder; diarrhoea; renal failure;  
KW muscular disorder; myocarditis; Duchenne's muscular dystrophy; noctropic;  
KW cardiovascular disorder; hypertension; bronchitis; vasculitis; cardiac;  
KW neurological disorder; Alzheimer's disease; Parkinson's disease; human;  
KW Huntington's disease; antiarteriosclerotic; hepatotoxic; cytotoxic;  
KW Anti-HIV; antianaemic; neuroprotective; immunomodulator; antidiabetic;  
KW hypotensive; vasotropic; antisthmatic; antiinflammatory; antidepressant;  
KW anticonvulsant; thrombolytic; antiParkinsonian; immunostimulant; ss.  
XX  
XX Homo sapiens.  
XX  
XX  
XX Key Location/Qualifiers  
XX CDS 364..1335  
XX /\*tag= a  
XX /product= "MECHP-12"  
XX FT 994..1041  
XX FT /\*tag= b  
XX FT /bound\_molecly= "Primer or Probe"  
XX  
XX WO200012711-A2.  
XX  
XX 09-MAR-2000.  
XX  
XX 02-SEP-1999; 99WO-US020468.  
XX  
XX 02-SEP-1998; 98US-0155226P.  
XX 12-NOV-1998; 98US-00191283.  
XX 09-DEC-1998; 98US-0155221P.  
XX 26-JAN-1999; 99US-0155211P.  
XX 10-FEB-1999; 99US-0155263P.  
XX  
XX (INCY-) INCYTE PHARM INC.  
XX  
XX Au-Young J, Bandman O, Tang YT, Reddy R, Hillman JL, Yye H;  
XX Lal P, Corley NC, Guegler KJ, Gorgone G, Baughn MR, Azimzal Y;  
XX WPI; 2000-256643/22.  
XX P-PSDB; AAY70462.  
XX  
XX Novel human membrane channel protein and polynucleotide useful for  
XX diagnosing and treating cell proliferative, inflammatory, secretory,  
XX osmoregulatory, muscular, cardiovascular and neurological disorders.  
XX  
XX Claim 9; Page 126; 140pp; English.  
XX  
XX  
XX The present sequence is a cDNA identified in Incyte clone 126774 derived  
XX from BRAINOT09 cDNA library. It encodes human membrane channel protein-12  
XX (MECHP-12), which is expressed in nervous tissues. Anti-MECHP antibodies  
XX can be used as therapeutic antagonists and reagents for diagnosis and  
XX monitoring diseases. MECHP cDNA can be used for diagnosis of MECHP-  
XX related diseases and gene mapping. MECHP can be used for treatment of  
XX cell proliferative disorders such as bursitis and atherosclerosis,  
XX cancers like lymphoma and sarcoma, inflammatory disorders like AIDS and  
XX Addison's disease, transport/secretory disorders like cystic fibrosis and  
XX diabetes mellitus, osmoregulatory disorders like diarrhoea and renal  
XX failure, muscular disorders like myocarditis and Duchenne's muscular  
XX dystrophy, cardiovascular disorders like hypertension and vasculitis,  
XX congenital lung anomalies like bronchitis and asthma and neurological  
XX disorders like Alzheimer's disease, Parkinson's disease and Huntington's  
XX disease  
XX  
XX  
SQ Sequence 1478 BP; 374 A; 416 C; 339 G; 349 T; 0 U; 0 Other;  
Query Match 8.3%; Score 54.4; DB 3; Length 1478;  
Best Local Similarity 70.2%; Pred. No. 0.00041;  
Matches 73; Conservative 0; Mismatches 31; Indels 0; Gaps 0;  
OY 218 GTGTGAAAAGGCGCTTCACTGACACCATCGGCGCTTGGGCT 277  
DB 372 GTTTATGAGAGGTTCCTCAATCTTTTAAACACCGTTGGTCTTGCGCTTCAAGCT 431  
OY 278 CATGACCATCGGCATCAGCATGACTACTGCTCTTACACAGAG 321

Db 432 GATGACCATAGCTGTGGAAACGACTATTGGCTCTACTCCAGAG 475

## RESULT 10

ID ABK51914 standard; cDNA; 1477 BP.

XX ABK51914;

XX 13-AUG-2002 (first entry)

XX cDNA encoding mouse Cacng3.

XX Mouse; neuronal voltage-gated calcium channel gamma subunit;

XX autoimmune disease; Lambert-Eaton syndrome; neuronal disease; epilepsy;

XX immunosuppressive; anticonvulsant; Cacng3; gene; ss.

XX Murinae gen. sp.

XX OS

XX Key Location/Qualifiers

XX 5'UTR 1.487

XX CDS /tag= a

XX /tag= b

XX /product= "Cacng3"

XX 3'UTR 1436.1477

XX /tag= c

XX US6365337-B1.

XX 02-APR-2002.

XX 27-JUL-1998; 98US-00123030.

XX 27-JUL-1998; 98US-00123030.

XX (IOWA ) UNIV IOWA RES FOUND.

XX (JACK-) JACKSON LAB.

XX Lette VA, Frankel WN, Campbell KP, Felix R, Biddlecome G;

XX WPI; 2002-433421/46.

XX P-PSDB; AAU97154.

XX Novel nucleic acid sequences encoding a neuronal voltage-gated calcium

XX channel gamma subunit useful in screening for compounds which modulate

XX activity of the channel and in diagnosing, treating neuronal diseases.

XX PS Disclosure; Fig 6; 36pp; English.

XX CC The present invention relates to the isolation of mouse genes encoding

XX CC neuronal voltage-gated calcium channel gamma subunits designated Cacng2,

XX CC Cacng3, and Cacng4. The genes are useful for identifying candidate

XX CC compounds for modulating the activity of human neuronal voltage-gated

XX CC calcium channels. They are also useful for diagnosing and treating the

XX CC autoimmune disease Lambert-Eaton syndrome, as well as diagnosing defects

XX CC in gamma subunit genes of a patient with a neuronal disease such as

XX CC epilepsy. The present sequence encodes mouse Cacng3

SQ Sequence 1477 BP; 352 A; 449 C; 356 G; 320 T; 0 U; 0 Other;

Query Match 8.2%; Score 53.6; DB 6; Length 1477;

Best Local Similarity 66.4%; Pred. No. 0.00067;

Matches 77; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Qy 218 GTGTGAAAAGGCGTTCAAGTACTGACACCATCGGCGCTTGGCGCTTGGCGCT 277

Db 496 GTGTGACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 555

Qy 278 CATGACCATCGCATCAGCATGACTACTGCTTACACAAAGCTTCATCTGCA 333

Db 556 AATGACCATTTGACAGTGGGACGAGCTAATGCTATATTCAGAGGTGTGTGACAGA 611

## RESULT 11

ID ABK51913 standard; cDNA; 1558 BP.

XX ABK51913;

XX 13-AUG-2002 (first entry)

XX cDNA encoding mouse Cacng2.

XX Mouse; neuronal voltage-gated calcium channel gamma subunit;

XX autoimmune disease; Lambert-Eaton syndrome; neuronal disease; epilepsy;

XX immunosuppressive; anticonvulsant; Cacng2; gene; ss.

XX Murinae gen. sp.

XX OS

XX Key Location/Qualifiers

XX 5'UTR 1.389

XX CDS /tag= a

XX /tag= b

XX /product= "Cacng2"

XX 3'UTR 1362.1558

XX /tag= c

XX US6365337-B1.

XX 02-APR-2002.

XX 27-JUL-1998; 98US-00123030.

XX 27-JUL-1998; 98US-00123030.

XX (IOWA ) UNIV IOWA RES FOUND.

XX (JACK-) JACKSON LAB.

XX Lette VA, Frankel WN, Campbell KP, Felix R, Biddlecome G;

XX WPI; 2002-433421/46.

XX P-PSDB; AAU97153.

XX Novel nucleic acid sequences encoding a neuronal voltage-gated calcium

XX channel gamma subunit useful in screening for compounds which modulate

XX activity of the channel and in diagnosing, treating neuronal diseases.

XX PS Claim 2; Fig 2; 36pp; English.

XX CC The present invention relates to the isolation of mouse genes encoding

XX CC neuronal voltage-gated calcium channel gamma subunits designated Cacng2,

XX CC Cacng3, and Cacng4. The genes are useful for identifying candidate

XX CC compounds for modulating the activity of human neuronal voltage-gated

XX CC calcium channels. They are also useful for diagnosing and treating the

XX CC autoimmune disease Lambert-Eaton syndrome, as well as diagnosing defects

XX CC in gamma subunit genes of a patient with a neuronal disease such as

XX CC epilepsy. The present sequence encodes mouse Cacng2

SQ Sequence 1558 BP; 418 A; 441 C; 360 G; 339 T; 0 U; 0 Other;

Query Match 8.0%; Score 52.8; DB 6; Length 1558;

Best Local Similarity 69.2%; Pred. No. 0.0011;

Matches 72; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 218 GTGTGAAAAGGCGTTCAAGTACTGACACCATCGGCGCTTGGCGCTTGGCGCT 277

Db 398 GTTGTGACAGAGTGTTCAAATGCTTTTAAACACCGTGTGCTTTCGCTTCAAGCTT 457

Qy 278 CATGACCATCGCATCAGCATGACTACTGCTTACACAAAGCTTCATCTGCA 321

Db 458 GATGACCATCGCTGTGGAAACGAGCTAATGCTATATTCAGAGGTGTGTGACAGA 501

## RESULT 12



```

AA299794
ID AA299794 standard; DNA; 945 BP.
XX
AC AA299794;
XX
DT 12-JUL-2000 (first entry)
XX
DE EST corresponding to a neuronal voltage-gated calcium channel DNA.
XX
KW Human; neuronal voltage-gated calcium channel; gamma-2 subunit;
KW gamma-3 subunit; CACNG1K2; neurological disorder; epilepsy; stroke;
KW head trauma; migraine; affective disorder; depression; anxiety;
KW schizophrenia; neurodegenerative disorder; Alzheimer's disease;
KW cognitive disorder; pain; cancer; vaccine; expressed sequence tag; EST;
KW ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..945
FT /*tag= a
XX
PN WO200014225-A1.
XX
PD 16-MAR-2000.
XX
PE 06-SEP-1999; 99WO-GB002945.
XX
PR 08-SEP-1998; 98GB-00019589.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Duckworth DM, Hayes PD;
XX
DR WPI: 2000-256977/22.
XX
P-PSDB; AAY84375.
XX
PT CACNG1K2 polynucleotides and polypeptides, useful in diagnostic assays
PT and for treating conditions such as Alzheimer's.
XX
PS Claim 11; Page 31; 33pp; English.
XX
CC The present sequence represents an expressed sequence tag (EST)
CC corresponding to a putative human neuronal voltage-gated calcium channel
CC gamma-2 and gamma-3 subunit, designated CACNG1K2 polypeptides. The
CC CACNG1K2 polynucleotide and polypeptide are useful for treating
CC neurological disorders, epilepsies, stroke, head trauma, migraine,
CC affective disorders including depression and anxiety, schizophrenia,
CC neurodegenerative disorders including Alzheimer's disease, cognitive
CC disorders, pain and cancer. They may also be used to configure screening
CC methods for detecting the effect of added compounds on the production of
CC mRNA in cells. The polypeptides may also be used as vaccines to induce an
CC immunological response in mammals
XX
SQ Sequence 945 BP; 232 A; 274 C; 217 G; 222 T; 0 U; 0 Other;
XX
Query Match 7.9%; Score 52; DB 3; Length 945;
Best Local Similarity 65.5%; Pred. No. 0.0015;
Matches 76; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
OY 218 GTGTGAAGAGGCGTTGAGTACTGACCACTGCGCGCTTTGGCGCT 277
DB 9 GTGTGACAGAGGTATCCAGATGTTGATCCACCTAGAGAGCTTTGCCGCTTTAGTTT 68
OY 278 CATGACCATTCGCATCAGACTGACTGCTCTACACAGAGCTTCATCTGCA 333
DB 69 AATGACCATTTGAGTGGCAGCAGGACTACTGTTATATTCAGAGGTGTGTGACAGA 124

```

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AC AA299793;
XX
DT 12-JUL-2000 (first entry)
XX
DE DNA encoding a neuronal voltage-gated calcium channel.
XX
KW Human; neuronal voltage-gated calcium channel; gamma-2 subunit;
KW gamma-3 subunit; CACNG1K2; neurological disorder; epilepsy; stroke;
KW head trauma; migraine; affective disorder; depression; anxiety;
KW schizophrenia; neurodegenerative disorder; Alzheimer's disease;
KW cognitive disorder; pain; cancer; vaccine; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..948
FT /*tag= a
FT /product= "voltage-gated calcium channel"
XX
PN WO200014225-A1.
XX
PD 16-MAR-2000.
XX
PE 06-SEP-1999; 99WO-GB002945.
XX
PR 08-SEP-1998; 98GB-00019589.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Duckworth DM, Hayes PD;
XX
DR WPI: 2000-256977/22.
XX
P-PSDB; AAY84374.
XX
PT CACNG1K2 polynucleotides and polypeptides, useful in diagnostic assays
PT and for treating conditions such as Alzheimer's.
XX
PS Claim 4; Page 29; 33pp; English.
XX
CC The present sequence encodes a putative human neuronal voltage-gated
CC calcium channel gamma-2 and gamma-3 subunit, designated CACNG1K2
CC polypeptides. The CACNG1K2 polynucleotide and polypeptide are useful
CC for treating neurological disorders, epilepsies, stroke, head trauma,
CC migraine, affective disorders including depression and anxiety,
CC schizophrenia, neurodegenerative disorders including Alzheimer's disease,
CC cognitive disorders, pain and cancer. They may also be used to configure
CC screening methods for detecting the effect of added compounds on the
CC production of mRNA in cells. The polypeptides may also be used as
CC vaccines to induce an immunological response in mammals
XX
SQ Sequence 948 BP; 234 A; 273 C; 218 G; 223 T; 0 U; 0 Other;
XX
Query Match 7.9%; Score 52; DB 3; Length 948;
Best Local Similarity 65.5%; Pred. No. 0.0015;
Matches 76; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
OY 218 GTGTGAAGAGGCGTTGAGTACTGACCACTGCGCGCTTTGGCGCT 277
DB 9 GTGTGACAGAGGTATCCAGATGTTGATCCACCTAGAGAGCTTTGCCGCTTTAGTTT 68
OY 278 CATGACCATTCGCATCAGACTGACTGCTCTACACAGAGCTTCATCTGCA 333
DB 69 AATGACCATTTGAGTGGCAGCAGGACTACTGTTATATTCAGAGGTGTGTGACAGA 124

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RESULT 13
AA299793
ID AA299793 standard; DNA; 948 BP.
XX

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RESULT 14
ABA09004
ID ABA09004 standard; cDNA; 1383 BP.
XX
AC ABA09004;
XX
DT 11-JAN-2002 (first entry)
XX

```



DE Human voltage gated Cl channel subunit homologue cDNA, SEQ ID NO:780.  
 XX  
 XX Human; cytokine; cell proliferation; cell differentiation; growth factor;  
 KW haematopoietic regulation; tissue growth; immunomodulator; activin;  
 KW inhibin; chemokinesis; chemokinesis; thrombolytic; oncogenesis;  
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;  
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;  
 KW chronic inflammatory condition; proliferative retinopathy;  
 KW atherosclerosis; coronary heart disease; arterial ischaemia;  
 KW bone disorder; osteoporosis; vascular growth disorder;  
 KW tissue regeneration; wound healing; infection; immune disorder;  
 KW cell culture; drug screening; gene therapy; antiinflammatory;  
 KW antileukemic; antiarthritic; haemostatic; antiarteriosclerotic;  
 KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;  
 KW antifungal; vulnery; antilicer; ss.  
 XX  
 OS Homo sapiens.  
 PN WO200157188-A2.  
 PD 09-AUG-2001.  
 PF 05-FEB-2001; 2001WO-US003800.  
 PR 03-FEB-2000; 2000US-00496914.  
 PR 27-APR-2000; 2000US-00560875.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 PI Tang YT, Liu C, Drmanac RT;  
 XX  
 XX WPI; 2001-457740/49.  
 DR P-PSDB; ABB11760.  
 PT Human proteins and DNA encoding sequences useful for preventing, treating  
 or ameliorating a medical condition in a mammalian subject e.g. arthritis  
 and cancer.  
 PS  
 XX Claim 1, Page 691-692; 1963pp; English.  
 CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and  
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The  
 CC invention also relates to vectors and recombinant host cells comprising a  
 CC nucleotide of the invention, methods of producing the novel polypeptides,  
 CC antibodies against the polypeptides, methods of detecting the nucleotides  
 CC or polypeptides in a sample, and methods of identifying compounds which  
 CC bind to polypeptides of the invention. Although novel, many of the  
 CC polypeptides of the invention have homology to known proteins, thereby  
 CC giving an insight into their probable biological activities, and hence  
 CC potential therapeutic applications. The polypeptides of the invention may  
 CC have various activities, including cytokine, cell proliferation or cell  
 CC differentiation activities; stem cell growth factor activity;  
 CC haematopoietic regulatory activity; tissue growth activity;  
 CC immunomodulatory activity; activin- or inhibin-related activities;  
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or  
 CC thrombolytic activities; receptor or ligand activities; or may be  
 CC involved in oncogenesis, cancer cell proliferation or metastasis.  
 CC Depending on their biological activities, polypeptides and nucleotides of  
 CC the invention are useful for preventing, treating or ameliorating medical  
 CC conditions, e.g., by protein or gene therapy. Such conditions include  
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell  
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),  
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,  
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal  
 CC vascular growth. Polypeptides involved with tissue regeneration and  
 CC repair (or nucleic acids encoding them) may be used to promote wound  
 CC healing (e.g., of burns, incisions and ulcers), while those with  
 CC immunomodulatory activities may be used in the treatment of viral,  
 CC bacterial and fungal infections in addition to immune disorders.  
 CC Polypeptides with growth factor activity may be used in cell cultures to  
 CC promote cell growth. For example, such polypeptides may be used to  
 CC manipulate stem cells in culture to give rise to neuroepithelial cells  
 CC that can be used to augment or replace cells damaged by illness,

CC autoimmune disease or accidental damage. The polypeptides and nucleotides  
 CC may also be used in the diagnosis of the above conditions, and in drug  
 CC screening techniques. The present sequence represents a cDNA encoding a  
 CC novel human polypeptide of the invention  
 XX  
 SQ Sequence 1383 BP; 336 A; 407 C; 341 G; 299 T; 0 U; 0 Other;  
 Query Match 7.9%; Score 52; DB 4; Length 1383;  
 Best Local Similarity 65.5%; Pred. No. 0.0017;  
 Matches 76; Conservative 0; Mismatches 40; Indels 0; Gaps 0;  
 QY 218 GGTGAAAAGGCGCTTCACTGATCACTGACCACTGGCGCTTGGCGCTTGGCCT 277  
 DB 429 GGTGACAGAGGTATCCAGATGTGATGACCACTGAGAGCGCTTGGCTTTAGTTT 488  
 QY 278 CATGACCATGCCCATCAGCATGACTGACTGCTCTACAAAGCTCTATCTGCA 333  
 DB 489 AATGACCATTTGACGTGGCAGCGACTACTGTTTATTTCCAGAGGTGTGACAGA 544  
 RESULT 15  
 AACT7216  
 ID AACT7216 standard; cDNA; 1854 BP.  
 XX  
 AC AACT7216;  
 XX  
 DT 08-FEB-2001 (first entry)  
 XX  
 DE Human ORFX ORF2771 polynucleotide sequence SEQ ID NO:5541.  
 XX  
 KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;  
 KW vulnery; antiparkinsonian; antiparkinsonian; neuroprotective;  
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;  
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
 KW hypotensive; dermatological; immunosuppressive; antiinflammatory;  
 KW antiviral; antibacterial; antifungal; antineumatic; antihypertoid;  
 KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;  
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;  
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;  
 KW cholesterol ester storage; systemic lupus erythematosus; infection;  
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
 KW bone damage; cartilage damage; antiinflammatory disease; coagulation;  
 KW thrombosis; contraceptive; ss.  
 XX  
 OS Homo sapiens.  
 PN WO200058473-A2.  
 PD 05-OCT-2000.  
 PF 31-MAR-2000; 2000WO-US008621.  
 PR 31-MAR-1999; 99US-0127607P.  
 PR 02-APR-1999; 99US-0127636P.  
 PR 05-APR-1999; 99US-0127728P.  
 PR 30-MAR-2000; 2000US-00540763.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 PI Shinkets RA, Leach M;  
 XX  
 DR WPI; 2000-602362/57.  
 DR P-PSDB; AAB43007.  
 PT Novel nucleic acids and peptides derived from open reading frame X,  
 PT useful for treating e.g. cancers, proliferative disorders,  
 PT neurodegenerative disorders and cardiovascular disease.  
 PS Claim 5; Page 4724-4725; 5507pp; English.  
 XX  
 CC AACT7446 to AACT7506 encode the proteins given in AAB40237 to AAB43397,  
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX

CC sequences have activities such as: cytostatic; hepatotropic; vulnery; antiparasitic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; CC adiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; CC dermatological; immunosuppressive; antiinflammatory; antibacterial; CC antiviral; antifungal; antineumatic; antithyroid; and antianaemic. The CC sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORF-associated disorder. The nucleic acids can be used to express ORF proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive

XX Sequence 1854 BP; 460 A; 549 C; 414 G; 429 T; 0 U; 2 Other;

Query Match 7.9%; Score 52; DB 3; Length 1854;

Best Local Similarity 65.5%; Pred. No. 0.0019; Mismatches 40; Indels 0; Gaps 0;

Matches 76; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Qy 218 GTGTGAAAAGGCGTTCAAGTACTGACCAACATCGGCGCTTGGCGCTTTGGCCT 277  
 |||||  
 Db 354 GTGTGACAGAGGTATCCAGATGTTGATCCACACTGAGAGCGCTTGCCGCTTTAGTTT 413  
 |||||  
 Qy 278 CATGACCATCGGCATCAGACTGACTAGCTCTACACAGAGCTTCATCTGCA 333  
 |||||  
 Db 414 AATGACCATTCAGTGGCAGCGACTACTGTTATATTCCAGAGGTGTGTGCAGGA 469  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)  
8276.126 Million cell updates/sec

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Perfect score: 656

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*  
1: em\_estb1:\*  
2: em\_estb2:\*  
3: em\_estb3:\*  
4: em\_estb4:\*  
5: em\_estb5:\*  
6: em\_estb6:\*  
7: em\_estb7:\*  
8: em\_estb8:\*  
9: em\_estb9:\*  
10: em\_estb10:\*  
11: em\_estb11:\*  
12: em\_estb12:\*  
13: em\_estb13:\*  
14: em\_estb14:\*  
15: em\_estb15:\*  
16: em\_estb16:\*  
17: em\_estb17:\*  
18: em\_estb18:\*  
19: em\_estb19:\*  
20: em\_estb20:\*  
21: em\_estb21:\*  
22: em\_estb22:\*  
23: em\_estb23:\*  
24: em\_estb24:\*  
25: em\_estb25:\*  
26: em\_estb26:\*  
27: em\_estb27:\*  
28: em\_estb28:\*  
29: em\_estb29:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	644	98.2	656	29	CG591004 OST245090
2	474	72.3	504	29	CG601451 OST273800
3	452	68.9	478	29	CG65024 OST452876
4	332.4	50.7	337	10	BE647856 UI-M-BH1-BE647856

Result No.	Score	Query Match	Length	ID	Description
5	234.2	35.7	558	13	BQ266161 NISC f411
6	189.6	28.9	547	10	BE102334 UI-R-BH1-BE102334
7	174	26.5	245	10	BE664111 UI-M-BH1-BE664111
8	159.8	24.4	663	10	BE641732 UI-M-BH1-BE641732
9	155.8	23.8	472	9	AW060348 UI-M-BH1-AW060348
10	121.2	18.5	169	29	CG620013 OST1316577
11	102.2	15.6	983	29	CG591004 OST245090
12	92	14.0	655	14	CD15523 ppp2n.pk0
13	86.4	13.2	528	14	CK332731 H8212B12-BG803929
14	86.4	13.2	600	12	BE803929 0243-54 M
15	86.4	13.2	961	14	CF583776 AGENCOURT
16	83.6	12.7	600	13	BU925588 7124-20 M
17	81.8	12.5	594	12	BI981765 f414905.Y
18	81.4	12.4	587	12	BI844628 Tetradon
19	74.4	11.3	999	29	CNS04474 CNS04474
20	73.6	11.2	691	12	BE912818 F.rubrip
21	73.6	11.2	697	13	BY733596 F.rubrip
22	73.2	11.2	592	29	FR0019468 F.rubrip
23	62	9.5	615	29	CNS04174 CNS04174
24	61.4	9.4	687	29	CNS04174 CNS04174
25	61.4	9.4	688	10	BE212599 Tetradon
26	61.4	9.4	697	10	BE574164 IPBm0032
27	61.4	9.4	877	14	CA496554 AGENCOURT
28	58.2	8.9	771	14	CA750036 UI-M-FD0-CA750036
29	56	8.5	923	29	CNS021DK CNS021DK
30	54.4	8.3	575	29	FR0019451 F.rubrip
31	54.4	8.3	580	10	BE222518 h92c08.x
32	54.4	8.3	599	9	A1912567 w61b12.x
33	54.4	8.3	606	10	BE670632 AK045362
34	54.4	8.3	640	10	AK045362 Mus muscu
35	54.4	8.3	2427	11	AK045362 Mus muscu
36	53.6	8.2	1043	29	CNS03MBE CNS03MBE
37	53.6	8.2	514	13	BM951619 UI-M-BH1-BM951619
38	53.6	8.2	649	12	BI739481 603361722
39	53.6	8.2	855	12	BI739481 603361722
40	53.6	8.2	948	29	AY411029 Mus muscu
41	53.6	8.2	1103	13	AX403654 BX403654
42	53.4	8.1	157	9	A1693801 w487a03.x
43	53.4	8.1	965	12	BI457751 603198193
44	53	8.1	1345	28	CC273194 CH261-37J
45	52.8	8.0	477	10	BE61331 UI-M-AKO-BE61331

#### ALIGNMENTS

RESULT 1  
LOCUS CG591004 656 bp DNA linear GSS 02-OCT-2003  
DEFINITION OST245090 Mus musculus 129SV/Ev Mus musculus genomic clone  
ACCESSION CG591004  
VERSION CG591004.1 GI:37398453  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Bases 1 to 656)

AUTHORS Zambrowicz, B.P., Abuh, A., Ramirez-Solis, R., Richter, L.J., Pliginsk, J., Beltrando, R.H., Buxton, E.C., Edwards, J., Finch, R.A., Fridolf, C., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jiang, C., Key, B.W., Jr., Kipp, P., Kohlschütter, B., Ma, Z.-Q., Marzessich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schick, J., Shi, Z.-Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T.  
Mkl kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)  
Contact: Zambrowicz BP  
Omnibank  
Lexicon Genetics Incorporated  
4000 Research Forest Drive, The Woodlands, TX 77381, USA

Email: material@lexgen.com  
Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)  
Class: Gene Trap.

FEATURES  
source location/Qualifiers

1..656  
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/db\_xref="taxon:10090"  
/clone="OST245090"  
/cell\_type="embryonic stem cell"  
/clone\_lib="Mus musculus 129SV/Ev"

ORIGIN

Query Match 98.2%; Score 644; DB 29; Length 656;  
Best Local Similarity 100.0%; Pred. No. 3.3e-122; Indels 0; Gaps 0;  
Matches 656; Conservative 0; Mismatches 0;

Qy 1 TATGCTTCACTCTGACACTTGGCTTGCAGCAACCTGCTGCTGCCCGCCCGCCCTC 60  
Db 1 TATGCTTCACTCTGACACTTGGCTTGCAGCAACCTGCTGCTGCCCGCCCGCCCTC 60  
Qy 61 TGGCCCTTGAAGGCCGCCAGCTTCTGCTGCTGTGATCCGCCAGCCGCGACAG 120  
Db 61 TGGCCCTTGAAGGCCGCCAGCTTCTGCTGCTGTGATCCGCCAGCCGCGACAG 120  
Qy 121 CCCGCTCCGCTGCGCGGTGTGGCCAGCGCCCGCGGTGTGCAGTGTGAATCTGG 180  
Db 121 CCCGCTCCGCTGCGCGGTGTGGCCAGCGCCCGCGGTGTGCAGTGTGAATCTGG 180  
Qy 181 AGTCATTGAAAAGCTGGAATGAAGAAGGGGTTTGTGTGTGTAAGGAGGCGTTCA 240  
Db 181 AGTCATTGAAAAGCTGGAATGAAGAAGGGGTTTGTGTGTGTAAGGAGGCGTTCA 240  
Qy 241 TACTGACCAACATCGCGCTTTCGCGGCTTTTGGCTTATGATGATCCCATCAG 300  
Db 241 TACTGACCAACATCGCGCTTTCGCGGCTTTTGGCTTATGATGATCCCATCAG 300  
Qy 301 ACTATGCTGTACAAAGAGCTCATCTGCAACCAACCAACCTCAAGAGGTGATG 360  
Db 301 ACTATGCTGTACAAAGAGCTCATCTGCAACCAACCAACCTCAAGAGGTGATG 360  
Qy 361 ACGGACCAACCCATGTGGGGGAGTGTGCTCTCCGAGAAGAGACCTGTGGGCTCA 420  
Db 361 ACGGACCAACCCATGTGGGGGAGTGTGCTCTCCGAGAAGAGACCTGTGGGCTCA 420  
Qy 421 CACATTCAGGCTCTGGCGGATATGCTGCTGGAAGTATGGGTGCAAGAGGCTGCT 480  
Db 421 CACATTCAGGCTCTGGCGGATATGCTGCTGGAAGTATGGGTGCAAGAGGCTGCT 480  
Qy 481 GGGCAGCTCCGNTGAAGCTGTGCTTNCAGCAATCGAATTATGTTCTGAGTCTAA 540  
Db 481 GGGCAGCTCCGNTGAAGCTGTGCTTNCAGCAATCGAATTATGTTCTGAGTCTAA 540  
Qy 541 CCCAAGNCTTGAAGGGGTGTGCTTTACTGCTGAGAGCGGNTAATTCATGACCCCTCA 600  
Db 541 CCCAAGNCTTGAAGGGGTGTGCTTTACTGCTGAGAGCGGNTAATTCATGACCCCTCA 600  
Qy 601 TNCCTNTTACAAATCCCTCTTCTGGGGAATTNCTGTTATTTTATTTCTTTG 656  
Db 601 TNCCTNTTACAAATCCCTCTTCTGGGGAATTNCTGTTATTTTATTTCTTTG 656

RESULT 2  
CG601451 504 bp DNA linear GSS 02-OCT-2003  
LOCUS OST273800 Mus musculus 129SV/Ev Mus musculus genomic clone  
DEFINITION OST273800, genomic survey sequence.  
ACCESSION CG601451  
VERSION CG601451.1 GI:37420111  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 504)

REFERENCE

Zambrowicz B.P., Abuin A., Ramirez-Soles R., Richter L.J.,  
Piggott J., Beltranderio H., Buxton E.C., Edwards J., Finch R.A.,  
Fridde C.J., Gupta A., Hansen G., Hu Y., Huang W., Jaling C.,  
Key B.W. Jr., Klipp P., Kohlfu B., Ma Z.-Q., Markesich D.,  
Payne R., Potter D.G., Qian N., Shaw J., Schrick J., Shi Z.-Z.,  
Spark M.J., Van Sligtenhorst I., Vogel P., Walke W., Xu N.,  
Zhu Q., Person C. and Sands A.T.  
Mx1 kinase deficiency lowers blood pressure in mice: a gene trap  
screen to identify potential targets for therapeutic intervention  
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)  
Contact: Zambrowicz BP

COMMENT

OmniBank  
Lexicon Genetics Incorporated  
4000 Research Forest Drive, The Woodlands, TX 77381, USA  
Email: material@lexgen.com  
Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)  
Class: Gene Trap.

FEATURES

source location/Qualifiers  
1..504  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="129SV/Ev"  
/db\_xref="taxon:10090"  
/clone="OST273800"  
/cell\_type="embryonic stem cell"  
/clone\_lib="Mus musculus 129SV/Ev"

ORIGIN

Query Match 72.3%; Score 474; DB 29; Length 504;  
Best Local Similarity 99.8%; Pred. No. 3e-87; Indels 1; Gaps 1;  
Matches 485; Conservative 0; Mismatches 0;

Qy 1 TATGCTTCACTCTGACACTTGGCTTGCAGCAACCTGCTGCTGCCCGCCCGCCCTC 60  
Db 1 TATGCTTCACTCTGACACTTGGCTTGCAGCAACCTGCTGCTGCCCGCCCGCCCTC 60  
Qy 15 TATGCTTCACTCTGACACTTGGCTTGCAGCAACCTGCTGCTGCCCGCCCGCCCTC 73  
Db 15 TATGCTTCACTCTGACACTTGGCTTGCAGCAACCTGCTGCTGCCCGCCCGCCCTC 73  
Qy 61 TGGCCCTTGAAGGCCGCCAGCTTCTGCTGCTGTGATCCGCCAGCCGCGACAG 120  
Db 61 TGGCCCTTGAAGGCCGCCAGCTTCTGCTGCTGTGATCCGCCAGCCGCGACAG 120  
Qy 74 TGGCCCTTGAAGGCCGCCAGCTTCTGCTGCTGTGATCCGCCAGCCGCGACAG 133  
Db 74 TGGCCCTTGAAGGCCGCCAGCTTCTGCTGCTGTGATCCGCCAGCCGCGACAG 133  
Qy 121 CCCGCTCCGCTGCGCGGTGTGGCCAGCGCCCGCGGTGTGCAGTGTGAATCTGG 180  
Db 121 CCCGCTCCGCTGCGCGGTGTGGCCAGCGCCCGCGGTGTGCAGTGTGAATCTGG 180  
Qy 134 CCCGCTCCGCTGCGCGGTGTGGCCAGCGCCCGCGGTGTGCAGTGTGAATCTGG 193  
Db 134 CCCGCTCCGCTGCGCGGTGTGGCCAGCGCCCGCGGTGTGCAGTGTGAATCTGG 193  
Qy 181 AGTCATTGAAAAGCTGGAATGAAGAAGGGGTTTGTGTGTGTAAGGAGGCGTTCA 240  
Db 181 AGTCATTGAAAAGCTGGAATGAAGAAGGGGTTTGTGTGTGTAAGGAGGCGTTCA 240  
Qy 241 TACTGACCAACATCGCGCTTTCGCGGCTTTTGGCTTATGATGATCCCATCAG 300  
Db 241 TACTGACCAACATCGCGCTTTCGCGGCTTTTGGCTTATGATGATCCCATCAG 300  
Qy 301 ACTATGCTGTACAAAGAGCTCATCTGCAACCAACCAACCTCAAGAGGTGATG 360  
Db 301 ACTATGCTGTACAAAGAGCTCATCTGCAACCAACCAACCTCAAGAGGTGATG 360  
Qy 361 ACGGACCAACCCATGTGGGGGAGTGTGCTCTCCGAGAAGAGACCTGTGGGCTCA 420  
Db 361 ACGGACCAACCCATGTGGGGGAGTGTGCTCTCCGAGAAGAGACCTGTGGGCTCA 420  
Qy 421 CACATTCAGGCTCTGGCGGATATGCTGCTGGAAGTATGGGTGCAAGAGGCTGCT 480  
Db 421 CACATTCAGGCTCTGGCGGATATGCTGCTGGAAGTATGGGTGCAAGAGGCTGCT 480  
Qy 481 GGGCAGCTCCGNTGAAGCTGTGCTTNCAGCAATCGAATTATGTTCTGAGTCTAA 540  
Db 481 GGGCAGCTCCGNTGAAGCTGTGCTTNCAGCAATCGAATTATGTTCTGAGTCTAA 540  
Qy 494 GGGCAGCTCCGNTGAAGCTGTGCTTNCAGCAATCGAATTATGTTCTGAGTCTAA 540  
Db 494 GGGCAGCTCCGNTGAAGCTGTGCTTNCAGCAATCGAATTATGTTCTGAGTCTAA 540



QY 77 CCCAGCTTGTGCTGTGTGATTCGCCAGCCGCGGACGAGCCCGCTCGCTGCC 136  
 DB 64 CCCAGCTTGTGCTGTGTGATTCGCCAGCCGCGGACGAGCCCGCTCGCTGCC 123  
 QY 137 CCGGTGTGGCCCAAGGCCCCCGGTGGTGCATGTGTGAACCTGATCTTGAACGCTG 196  
 DB 124 CCGGTGTGGCCCAAGGCCCCCGGTGGTGCATGTGTGAACCTGATCTTGAACGCTG 183  
 QY 197 GAATGAAGAGAGGGGTTTGTGTGTGAAGAGGCGTTGAGTACTACTGACCAACGCTG 256  
 DB 184 GAATGAAGAGAGGGGTTTGTGTGTGAAGAGGCGTTGAGTACTACTGACCAACGCTG 243  
 QY 257 GCGCTTCGGGGCTTTTGGCTTCATGACCATCGCATGAGCTGACTGCTCTTACAC 316  
 DB 244 GCGCTTCGGGGCTTTTGGCTTCATGACCATCGCATGAGCTGACTGCTCTTACAC 303  
 QY 317 AAGAGCTCTCATCTGCACACACCAACCTCACA 350  
 DB 304 AAGAGCTCTCATCTGCACACCAACCTCACA 337

## RESULT 5

LOCUS B0266161 558 bp mRNA linear EST 07-MAY-2002  
 DEFINITION B0266161 NISC\_f111c05.x1 NCI\_CGAP\_Mam5 Mus musculus cDNA clone IMAGE:2865416  
 3', mRNA sequence.  
 ACCESSION B0266161  
 VERSION B0266161.1 GI:20491226  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 558)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-rmail.nih.gov  
 Tissue Procurement: Lothar Hennighausen/Robin Humphreys  
 cDNA Library Preparation: Life Technologies  
 cDNA Library Arrayed By: The I.M.A.G.E. Consortium/LINL  
 DNA Sequencing By: National Institutes of Health Intramural  
 Sequencing Center (NISC)  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LINL at:  
 info@image.lnl.gov  
 MGI:1046188  
 Plate: LLMW7069 row: F column: 9  
 Seq primer: 21M13 forward primer (ABI).  
 Location/Qualifiers  
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 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:2865416"  
 /tissue\_type="tumor, gross tissue"  
 /dev\_stage="7 months"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI\_CGAP Mam5"  
 /note="Organ: mammary; Vector: PCMV-SPOrt6; Site 1: SalI;  
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
 library constructed by Life Technologies. Investigators  
 providing samples: Lothar Hennighausen/Robin Humphreys,  
 NIH"

## FEATURES

source

## ORIGIN

Query Match 35.7%; Score 234.2; DB 13; Length 558;  
 Best Local Similarity 89.2%; Pred No. 6 5e-38;  
 Matches 256; Conservative 0; Mismatches 30; Indels 1; Gaps 1;

QY 370 CCATGCTGGGGGAGTGTGCTCTCCGAGAAAGAGACCTCGGGGGCTCAACATTGAG 429  
 DB 558 CCATGCTGGGGGAGTGTGCTCTCCGAGAAAGAGACCTCGGGGGCTCAACATTGAG 499  
 QY 430 GCGCTTGGCGGATATGCTGCTGAGAGGTAGGCTGCAGAGAGGCCCTGCTGGCCACCTC 489  
 DB 498 GCGCTTGGCGGATATGCTGCTGAGAGGTAGGCTGCAGAGAGGCCCTGCTGGCCACCTC 439  
 QY 490 CGNTGAAGCTGTGCTTCAGCAACCAATGCACTTNTAGTGTCTGAGTCTCAACCCAGGNC 549  
 DB 438 GCGTGAAGCTGTGCTTCAGCAACCAATGCACTTNTAGTGTCTGAGTCTCAACCCAGGNC 379  
 QY 550 TTGAGGGGTGTGCTTACTGCTGAGAGGCGATNATTCATGACCCCTCATNCTTNT 609  
 DB 378 TTGATGGGTGTGCTTACTGCTGAGAGGCGTGTGATTCATGACACCCCTCATNCTTNT 319  
 QY 610 ACAATCCCTTCTGCGGATTTNNGTATTTATTTTCTTTG 656  
 DB 318 -CCAATCCCTTCTGCGGATTTCTGTTTATTTTATTTACTGG 273

## RESULT 6

LOCUS BE102334 547 bp mRNA linear EST 13-JUN-2000  
 DEFINITION BE102334 UI-R-BT1-aq1-d-02-0-UI.s1 UI-R-BT1 Rattus norvegicus cDNA clone  
 UI-R-BT1-aq1-d-02-0-UI 3', mRNA sequence.  
 ACCESSION BE102334  
 VERSION BE102334.1 GI:8494433  
 KEYWORDS EST.  
 SOURCE Rattus norvegicus (Norway rat)  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 547)  
 Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 Genome Res. 6 (9), 791-806 (1996)  
 9704447  
 8889548  
 Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: bento-soares@uiowa.edu  
 The sequence contained an oligo-dT track that was present in the  
 oligonucleotide that was used to prime the synthesis of first  
 strand cDNA and therefore this may represent a bonafide poly A  
 tail. The sequence tag present in the cDNA between the NotI site  
 and the oligo-dT track served to identify it as a clone from the  
 normalized corpus-reticulum library cDNA library Preparation: M.B.  
 Soares Lab Clone distribution: clones will be available through  
 Research Genetics (www.reegen.com) The following repetitive  
 elements were found in this cDNA sequence: 147-294, >B3SINE/B2  
 Seq primer: M13 Forward  
 POLYA=yes  
 Location/Qualifiers  
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 /db\_xref="taxon:10116"  
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 /dev\_stage="adult"  
 /lab\_host="DH10B (Life Technologies)"  
 /clone\_lib="UI-R-BT1"  
 /note="Vector: pRT3D-Pac (Pharmacia) with a modified  
 polylinker; Site 1: Not I; Site 2: Eco RI; The library  
 UI-R-BT1 is a subtracted library derived from a mixture of  
 the following tissues: hippocampus, thalamus, mid-brain,

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 COMMENT

## FEATURES

source





RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugihara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamakata, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.

Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

e mouse tissues.

# FEATURES

## SOURCE

1. 663

/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

/clone="A830045A22"

/tissue\_type="cortex"

/dev\_stage="10 days neonate"

/lab\_host="DH10B"

/clone\_lib="RIKEN full-length enriched, 10 days neonate cortex"

/note="Site 1: SalI; Site 2: BamHI. cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer 15' GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3'. cDNA was prepared by using transposase thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence 15' GAGAGAGAGATCTGAGATTAATTAATCCCCCCCCC 3'. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLX I."

# ORIGIN

Query Match 24.4%; Score 159.8; DB 10; Length 663;  
Best Local Similarity 80.6%; Pred. No. 1,4e-22;  
Matches 199; Conservative 0; Mismatches 47; Indels 1; Gaps 1;

1 TATGCTTCACTCTGACCTTGGCTGACGACCTGCTGCTGCCCCGCGCCCTC 60  
Db TATGCTTCACTCTGACCTTGGCTGACGACCTGCTGCTGCCCCGCGCCATC 467

61 TGGCCCTTGAAGCCCCCAGCTTGTGCTGTGATCCCGCCAGCCGCGACGG 120  
Db TGGCCCTTGAAGCCCCCAGCTTGTGCTGTGATCCCGCCAGCCGCGTCAAG 527

468 TGGCCCTTGAAGCCCCCAGCTTGTGCTGTGATCCCGCCAGCCGCGTCAAG 527  
Qy CCCCCCTTGGCTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180

121 CCCCCCTTGGCTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180  
Db CCCCCCTTGGCTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 587

528 CCCCCCTTGGCTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 587  
Qy AGTCATTGAAAGCTGGAATGAAGAGAGGGGTTTGTGATGAAGAGCGTTCAAGTAC 240

181 AGTCATTGAAAGCTGGAATGAAGAGAGGGGTTTGTGATGAAGAGCGTTCAAGTAC 240  
Db AGTCATTGAAAGCTGGAATGAAGAGAGGGGTTTGTGATGAAGAGCGTTTATCGCT 647

241 TACTGAC 247  
Qy |||||  
Db TCCCGAC 654

RESULT 9  
AM060348/c

LOCUS AM060348 472 bp mRNA linear EST 04-OCT-1999  
DEFINITION UI-M-BH1-anh-c-12-0-UI.s1 NIH BMP M.S2 Mus musculus cDNA clone  
UI-M-BH1-anh-c-12-0-UI 3', mRNA sequence.

ACCESSION AM060348

VERSION AM060348.1 GI:6008099

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 472)  
Bonaldo, M.F., Lennon, G. and Soares, M.B.  
Normalization and subtraction: two approaches to facilitate gene discovery  
Genome Res. 6 (9), 791-806 (1996)

JOURNAL 97044477  
MEDLINE  
PUBMED 8889548

COMMENT Contact: Chin, H  
National Institute of Mental Health  
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD  
20892-9643, USA  
Tel: 301 443 1706  
Fax: 301 443 9890  
Email: msb@mail.nih.gov

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized hippocampus library cDNA Library Preparation: M.B. Soares Lab clone distribution: NIH BMP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMP cDNA clones, this record will be updated accordingly when that means is determined. The following repetitive elements were found in this cDNA sequence:  
150-287, >B3SINE/B2  
Seq primer: M13 Forward  
POLYA=yes.

# FEATURES

## SOURCE

1. 472

/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UI-M-BH1-anh-c-12-0-UI"

/dev\_stage="27-32 days"

/lab\_host="DH10B (Life Technologies)"

/clone\_lib="NIH BMP M.S2"

/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The NIH BMP M.S2 library is a subtracted library derived from NIH BMP M.S1, which in turn is a subtracted library derived from a mixture of normalized libraries from ten regions of the mouse brain (cerebellum, brain stem, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus). The driver used for subtraction consisted of a pool of 5,000 clones from the NIH BMP M.S1 library and a pool of 2,000 clones obtained from non-normalized and normalized mouse brain spinal cord libraries.  
TAG\_TISSUE=hypothalamus  
TAG\_LIB=NIH BMP M.S2  
TAG\_SEQ=CGGTA"

# ORIGIN

Query Match 23.8%; Score 155.8; DB 9; Length 472;  
Best Local Similarity 85.5%; Pred. No. 8.5e-22;  
Matches 177; Conservative 0; Mismatches 29; Indels 1; Gaps 1;

450 CTGAAGGTAGGTGACGAGAGCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 509  
Db CTGAAGGTAGGTGACGAGAGCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 413

QY 510 GCAGATGCACTTCTGAGTCTCAACCAAGGCTGAGGGGTGCTTACTG 569  
 DB 412 GCAAAATGCACTTCTGAGTCTCAACCAAGGCTGAGGGGTGCTTACTG 353  
 QY 570 CTGAGAGCGGATTCATGACCCCTCCATTCCTTATACAAATCCCTCTTCTGGGA 629  
 DB 352 CTGAGAGCGGATTCATGACCCCTCCATTCCTTATACAAATCCCTCTTCTGGGA 294  
 QY 630 TTTTNGTGTATTTTATTTTCTTTG 656  
 DB 293 TCTCGTTTATTTTATTTTATTTACTGG 267

RESULT 10  
 CG620013  
 LOCUS OSJ116577, Mus musculus 1295v/Bv Mus musculus genomic clone  
 DEFINITION CG620013  
 ACCESSION CG620013  
 VERSION CG620013.1 GI:37443862  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclirognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 169)  
 Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Piggett, J., Beltrando-Rio, H., Buxton, E.C., Edwards, J., Finch, R.A., Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jang, C., Key, B.W., Jr., Kipp, P., Kohlhauf, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schick, J., Shi, Z.-Z., Sparks, M.J., Van Slijkenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T.  
 Mnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention  
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)  
 CONTACT: Zambrowicz BP  
 OMIBank  
 Lexicon Genetics Incorporated  
 4000 Research Forest Drive, The Woodlands, TX 77381, USA  
 Email: materials@lexgen.com  
 Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature, 1998 Apr 9;392(6676):608-11)  
 Class: Gene Trap.

FEATURES  
 source  
 1..169  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="129SV/Bv"  
 /db\_xref="taxon:10090"  
 /clone="OSJ116577"  
 /cell\_type="embryonic stem cell"  
 /clone\_11b="Mus musculus 1295v/Bv"

ORIGIN  
 Query Match 18.5%; Score 121.2; DB 29; Length 169;  
 Best Local Similarity 94.2%; Pred. No. 9.3e-15;  
 Matches 145; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

QY 1 TATGGCTTCACTTGACCTTGGCTCTGACAGCACCTGCTGCTGCCCCGAGCCCTTC 60  
 DB 15 TATGGCTTCACTTG-TCCTTGGCTCTGACAGCACCTGCTGCTGCCCCGAGCCCTTC 73  
 QY 61 TGGCCCTTGAAGCCCCCAAGCTTCTGCTGCTGCTGATCCGCCAGCGCGGAC-G 119  
 DB 74 TGGCCCTTGAAGCCCCCAAGCTTCTGCTGCTGCTGATGCCAGCGCGGACAG 133  
 QY 120 GCCCGGCTCGGCTGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 153  
 DB 134 GCCCGGCTCGGCTGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 167

RESULT 11

CNS0489W  
 LOCUS CNS0489W 983 bp DNA linear GSS 01-SEP-2000  
 DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone 090615 of library G from Tetraodon nigroviridis, genomic survey sequence.  
 ACCESSION AL279005  
 VERSION AL279005.1 GI:8016339  
 KEYWORDS GSS; genome survey sequence.  
 SOURCE Tetraodon nigroviridis  
 ORGANISM Tetraodon nigroviridis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE  
 AUTHORS Roest Crollius, H., Jallion, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brothier, P., Quetier, F., Saurin, W. and Weissenbach, J.  
 Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence  
 Nat. Genet. 25 (2), 235-238 (2000)  
 JOURNAL 20296633  
 MEDLINE 10835645  
 PUBMED 10835645

REFERENCE  
 AUTHORS Roest Crollius, H., Jallion, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.  
 Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis  
 Genome Res. 10 (7), 939-949 (2000)  
 JOURNAL 20359837  
 MEDLINE 10899143  
 PUBMED 10899143

TITLE 3 (bases 1 to 983)  
 GENOSCOPE.  
 Direct Submisson  
 Submitted (12-Apr-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr  
 - Web : www.genoscope.cns.fr)  
 This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

FEATURES  
 source  
 1..983  
 /organism="Tetraodon nigroviridis"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:99883"  
 /clone="090615"  
 /clone\_11b="G"  
 /note="Genoscope sequence ID : C0B090A0D08LPI-end : T7"

ORIGIN  
 Query Match 15.6%; Score 102.2; DB 29; Length 983;  
 Best Local Similarity 67.5%; Pred. No. 1e-10;  
 Matches 168; Conservative 0; Mismatches 63; Indels 18; Gaps 1;

QY 214 TGTGTGTAAAGAGCGCTTCACTGACTACTGACCAACATGCGCGCTTCTTGG 273  
 DB 293 TGTGTGTAAAGAGCGCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 352  
 QY 274 GCGTATGACATGCGCATGACACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 333  
 DB 353 CCTGTATGCGTGGCATGCGCATGCGACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 412  
 QY 334 ACACACCAACTCAAGAGGTGATGACGACACACCCATGCTGCGGCGAGTGTCTCT 393  
 DB 413 ACAGCAGCGCAACTCAACCCAGAGAC-----TCACAGACACA 454  
 QY 394 CCGAAGAAAGACCTTGGGGCTTCAACATTTAGGCTTGGGGGATATCTGCTGG 453  
 DB 455 AAGACAAAGAGACCCCGGGCTTCAACCTGCGGCTTGGAGATCTGCTGCTGG 514  
 QY 454 AAGTAGGG 462

Db 515 AAGTACCG 523

RESULT 12  
CD215523

LOCUS  
DEFINITION  
CD215523 655 bp mRNA linear EST 20-MAY-2003  
ppp2n.pk008.b11 Normalized chicken pituitary/hypothalamus/pineal  
cDNA library (ppp2n) Gallus gallus cDNA clone ppp2n.pk008.b11 5'  
similar to gb|AK72510.1 (AY037891) calcium channel gamma 4 subunit  
(Gallus gallus), mRNA sequence.

ACCESSION  
CD215523  
VERSION  
CD215523.1 GI:30955522  
KEYWORDS  
EST.  
SOURCE  
Gallus gallus (chicken)  
ORGANISM  
Gallus gallus

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Porter, T.E. and Cogburn, L.A.  
Chicken ESTs from pituitary/hypothalamus/pineal gland  
Unpublished (2001)  
Contact: Larry A. Cogburn  
University of Delaware  
Townsend Hall, Newark, DE 19717, USA  
Tel: 302-831-1335  
Fax: 302-831-2822  
Email: cogburn@udel.edu, www.chickest.udel.edu.  
Location/Qualifiers  
1..655  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Commercial broiler chickens"  
/db\_xref="taxon:9031"  
/clone="ppp2n.pk008.b11"  
/sex="Male and Female"  
/tissue\_type="Pituitary gland/Hypothalamus/Pineal Gland"  
/dev\_stage="Embryonic (dl2,dl4,dl9); post-hatch (1,3,5,7,9 weeks)"  
/lab\_host="E. Coli EMDH10B"  
/clone\_id="Normalized chicken  
pituitary/hypothalamus/pineal cDNA library (ppp2n)"  
/note="Vector: pCMVSPORT6; Library made from equivalent  
pools of total RNA isolated from each tissue at different  
ages. Single pass sequencing from 5'-end"

ORIGIN

Query Match 14.0%; Score 92; DB 14; Length 655;  
Best Local Similarity 65.9%; Pred. No. 1.2e-08;  
Matches 162; Conservative 0; Mismatches 60; Indels 24; Gaps 1;

QY 214 TGTGTGTGAAAAGGCGTTTCAGTACTGACCAACATCGGCCCTTCGGCGCTTTG 273  
Db 37 TGTGTGTGACCGTGTGCGTCCAGATGCTGTCGACCAAGTGGGACCTTTCGCCGCTTCA 96  
QY 274 GCGTCATGACATGCGCATGACATGACTGCTGTACACAGAGCTCTCATCTCA 333  
Db 97 GCGTCATGCGCATGCGCATGCTGTACGACTGTGCTGTACGCGGACATCTCA 156  
QY 334 ACACACCAACCTCAAGAGGTGATGACGACACACCCCATGCTGGGGGCAAGTGGCTCT 393  
Db 157 ACGGACCAACATCAACGACGACATGACGAGGGGCGG----- 195  
QY 394 CCGAGAGAGGACCTGGGGGCTTCACATTCAGGCGCTTGGCGGATATGCTGG 453  
Db 196 ---CGAAGAAAGCGAGGGGCGACCTACGACATTCGGGGGCTTGAGAGATGCTGCTCG 252  
QY 454 AAGGTA 459  
Db 253 AAGGAA 258

RESULT 13  
CK332731  
LOCUS  
DEFINITION  
CK332731 528 bp mRNA linear EST 19-DEC-2003  
H8212B12-5 N1A Mouse Unique Gene Set Version 2 Mus musculus cDNA  
clone H8212B12 5', mRNA sequence.

ACCESSION  
CK332731  
VERSION  
CK332731.1 GI:40232323  
KEYWORDS  
EST.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
Contact: Dawood B. Dudekula  
Laboratory of Genetics  
National Institute on Aging/National Institutes of Health  
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
Email: cdna@igsun.grc.nia.nih.gov  
Plate: H8212 row: B column: 12  
Seg primer: M13 Reverse  
High quality sequence stop: 528  
POLY=A=NO.

FEATURES  
source  
1..528  
Location/Qualifiers  
1..528  
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/lab\_host="DH10B"  
/clone\_id="N1A Mouse Unique Gene Set Version 2"  
/note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2:  
NotI; Mouse cDNA project by the Laboratory of Genetics,  
National Institute on Aging (NIA), Intramural Research  
Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This  
clone is among a rearrayed set of 11,424 clones from more  
than 20 cDNA libraries."

ORIGIN

Query Match 13.2%; Score 86.4; DB 14; Length 528;  
Best Local Similarity 66.8%; Pred. No. 1.6e-07;  
Matches 123; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 214 TGTGTGTGAAAAGGCGTTTCAGTACTGACCAACATCGGCCCTTCGGCGCTTTG 273  
Db 98 TGCATGAGACGCGGGGCTGAGATGCTGTCGACAGCGCGGAGCTTCGCCGCTTCT 157  
QY 274 GCGTCATGACATGCGCATGACATGACTGCTGTACACAGAGCTCTCATCTCA 333  
Db 158 GCGTCATGCGCATGCGCATGCGACCGACTGCTGTATCTCAAGCGCGACATCTGCA 217  
QY 334 ACACACCAACCTCAAGAGGTATGACGACACACCCCATGCTGGGGGCAAGTGGCTCT 393  
Db 218 ACGGACCAACCTCAAGAGGTATGACGACAGCGCGCGCGGCTGCGGCGACCTCA 277  
QY 394 CCGA 397  
Db 278 CCGA 281

RESULT 14  
BG803929

LOCUS BG803929 600 bp mRNA linear EST 20-DEC-2001  
 DEFINITION 0243-54 Mouse E14.5 retina lambda ZAP II library Mus musculus cDNA,  
 mRNA sequence.  
 ACCESSION BG803928  
 VERSION BG803929.1 GI:17950842  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 600)  
 REFERENCE Mu, X., Zhao, S., Pershad, R., Hsieh, T.-F., Scarpa, A., Wang, S.W.,  
 White, R.A., Beremand, P.D., Thomas, T.L., Gan, L. and Klein, W.H.  
 Authors White, R.A., Beremand, P.D., Thomas, T.L., Gan, L. and Klein, W.H.  
 Title Gene expression in the developing mouse retina by EST sequencing  
 and microarray analysis  
 Journal Nucleic Acids Res. 29 (24), 4983-4993 (2001)  
 MEDLINE 21671825  
 PUBMED 11812828  
 COMMENT Contact: Klein WH  
 Department of Biochemistry and Molecular Biology  
 University of Texas M.D. Anderson Cancer Center  
 Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA  
 Tel: 713 792 3646  
 Fax: 713 790 0329.  
 FEATURES  
 source 1..600  
 Location/Qualifiers  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /issue\_type="neural retina"  
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 /clone\_1lb="Mouse E14.5 retina lambda ZAP II library"  
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 Best Local Similarity 66.8%; Pred. No. 1.7e-07;  
 Matches 123; Conservative 0; Mismatches 61; Indels 0; Gaps 0;  
 QY 214 TGTGCTGTGAAAGGCGCTTCACTACTGACCAACATCGCGGCTTGGCGCTTTG 273  
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 DB 91 TGGGATGGACCGCGGCTGCAATGCTGTGACCAAGCGCGGAGCTTGGCGCTTCT 150  
 QY 274 GCCTATGACCATCGCATGACATGATGCTGCTTCAACAAGAGCTCTCATCTGCA 333  
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 DB 151 CGCTATGGCATCGCATGCGCACCGACATCTGGCTGATCTCAAGCGGACATCTGCA 210  
 QY 334 ACACGACCAACCTTACAGCAGGATGATGACGACACCCCATCTGCGGGGAGATGCTCT 393  
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 DB 211 ACGGACCAACCTGACATGACGACGAGCGGCGCGCGCGCGCGCTCGGGGAGACTCTA 270  
 QY 394 CCGA 397  
 |||||  
 DB 271 CCGA 274

RESULT 15  
 CFS83776  
 LOCUS CFS83776 961 bp mRNA linear EST 24-SEP-2003  
 DEFINITION AGENCOURT\_11364559 updated NIH\_MGC\_137 Mus musculus cDNA clone  
 IMAGE:6431780 5', mRNA sequence.  
 ACCESSION CFS83776  
 VERSION CFS83776.1 GI:35197038  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 961)  
 REFERENCE NIH-MGC. <http://mgc.ncl.nih.gov/>.  
 Authors National Institutes of Health, Mammalian Gene Collection (MGC)  
 Title Unpublished (1999)  
 Journal Contact: Daniela S. Gerhard, Ph.D.  
 COMMENT Office of Cancer Genomics

National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
 Tissue Procurement: Gerard Gradwohl (PNAS 97 P1607-1611, 2000)  
 cDNA Library Preparation: Catherine Lee, Endocrine Pancreas  
 Consortium  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: IRBD19 row: h column: 09  
 High quality sequence stop: 551.  
 Location/Qualifiers  
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 /lab\_host="DH10B"  
 /clone\_1lb="NIH\_MGC\_137"  
 /note="Organ: pancreas; Vector: pSPORT1; Site\_1: SalI;  
 Site\_2: NotI; Library consists of a pool of clones  
 rearranged from the following libraries: Melton normalized  
 mixed mouse pancreas 1 NI-MMS1, Amplified Melton mouse  
 islets 1 MMS1-A, and Kaestner ngn3 wt. Clones rearranged in  
 the laboratory of K. Kaestner (University of  
 Pennsylvania). Note: this is a NIH\_MGC Library."

ORIGIN  
 Query Match 13.2%; Score 86.4; DB 14; Length 961;  
 Best Local Similarity 66.8%; Pred. No. 1.8e-07;  
 Matches 123; Conservative 0; Mismatches 61; Indels 0; Gaps 0;  
 QY 214 TGTGCTGTGAAAGGCGCTTCACTACTGACCAACATCGCGGCTTGGCGCTTTG 273  
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 DB 281 TGGGATGGACCGCGGCTGCAATGCTGTGACCAAGCGCGGAGCTTGGCGCTTCT 340  
 QY 274 GCCTATGACCATCGCATGACATGATGCTGCTTCAACAAGAGCTCTCATCTGCA 333  
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 DB 341 CGCTATGGCATCGCATGCGCACCGACATCTGGCTGATCTCAAGCGGACATCTGCA 400  
 QY 334 ACACGACCAACCTTACAGCAGGATGATGACGACACCCCATCTGCGGGGAGATGCTCT 393  
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 DB 401 ACGGACCAACCTGACATGACGACGAGCGGCGCGCGCGCGCTCGGGGAGACTCTA 460  
 QY 394 CCGA 397  
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 DB 461 CCGA 464

Search completed: May 22, 2004, 16:59:11  
 Job time : 2372 secs



Result No.	Score	Query Match	Length	DB	ID	Description
1	170.8	26.0	1091	10	US-09-945-527-9	Sequence 9, Appl1
2	96.4	14.7	1173	13	US-10-114-270-1	Sequence 1, Appl1
3	96.4	14.7	1173	13	US-10-403-161-27	Sequence 27, Appl
4	86.4	13.2	984	9	US-09-683-483-1	Sequence 1, Appl1
5	54.4	8.3	1252	13	US-10-276-774-825	Sequence 825, Appl
6	52.7	7.9	1383	13	US-10-276-774-780	Sequence 780, Appl
7	46.4	7.1	440	15	US-10-184-644-502	Sequence 202, Appl
8	46.4	7.1	440	15	US-10-184-634-402	Sequence 2, Appl
9	46.4	7.1	440	15	US-10-063-685-52	Sequence 52, Appl
10	45.8	7.0	956	13	US-10-027-632-11508	Sequence 11508, A
11	45.8	7.0	956	16	US-10-027-632-11508	Sequence 11508, A
12	44	6.7	497	13	US-10-424-589-133788	Sequence 133788, A
13	43.8	6.7	791	13	US-10-424-559-64474	Sequence 64474, A
14	43.6	6.6	451	13	US-10-240-425-721	Sequence 721, Appl

C 15	43.2	6.6	71.952	13	US-10-087-192-19445	Sequence 1942, A
C 16	43	6.5	80.295	13	US-10-434-599-61903	Sequence 61903, A
C 17	42.8	6.5	126	15	US-10-234-804-3	Sequence 3, Appl
C 18	42.8	6.5	8705	15	US-10-231-230-14	Sequence 14, Appl
C 19	42.8	6.5	8705	15	US-10-231-249-14	Sequence 14, Appl
C 20	42.8	6.5	8705	17	US-10-273-678-16	Sequence 16, Appl
C 21	42.8	6.5	9600	15	US-10-278-751-1	Sequence 1, Appl
C 22	42.8	6.5	10233	15	US-10-050-898-283	Sequence 283, Appl
C 23	42.8	6.5	10285	15	US-10-050-902-283	Sequence 283, Appl
C 24	42.4	6.5	8637	15	US-10-207-555-56	Sequence 56, Appl
C 25	42.2	6.4	615	13	US-10-282-122A-11845	Sequence 11845, A
C 26	41.6	6.3	10343	13	US-10-655-847-11	Sequence 11, Appl
C 27	41.6	6.3	10343	13	US-10-160-807-11	Sequence 11, Appl
C 28	41.6	6.3	594	13	US-10-142-426-10	Sequence 10, Appl
C 29	41.4	6.3	594	15	US-10-143-155-10	Sequence 10, Appl
C 30	41.4	6.3	594	15	US-10-146-731-10	Sequence 10, Appl
C 31	41.4	6.3	594	15	US-10-140-472-10	Sequence 10, Appl
C 32	41.4	6.3	594	15	US-10-141-761-10	Sequence 10, Appl
C 33	41.4	6.3	594	15	US-10-142-885-10	Sequence 10, Appl
C 34	41.4	6.3	594	15	US-10-158-790-10	Sequence 10, Appl
C 35	41.4	6.3	594	16	US-10-137-871-10	Sequence 10, Appl
C 36	41.4	6.3	594	16	US-10-140-923-10	Sequence 10, Appl
C 37	41.4	6.3	594	16	US-10-141-756-10	Sequence 10, Appl
C 38	41.4	6.3	594	16	US-10-141-759-10	Sequence 10, Appl
C 39	41.4	6.3	594	16	US-10-140-805-10	Sequence 10, Appl
C 40	41.4	6.3	594	16	US-10-140-864-10	Sequence 10, Appl
C 41	41.4	6.3	12733	15	US-10-032-393-47	Sequence 47, Appl
C 42	41.4	6.3	12733	15	US-10-032-393-47	Sequence 47, Appl
C 43	41.4	6.3	114793	15	US-10-148-806-3	Sequence 3, Appl
C 44	41.2	6.3	528	13	US-10-424-599-42496	Sequence 42496, A
C 45	41.2	6.3	804	13	US-10-424-599-100535	Sequence 100535, A

## ALIGNMENTS

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RESULT 1
US-09-945-527-9
; Sequence 9, Application US/09945527
; Publication No. US2003005588A1
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. US2003005588A1 Nucleic Acid Molecules Encoding
; FILE REFERENCE: 35800/237985
; CURRENT APPLICATION NUMBER: US/09/945,527
; CURRENT FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1091
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-945-527-9

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Query Match      26.0%;    Score 170.8;    DB 10;    Length 1091;

Matches 219; Conservative 0; Mismatches 52; Indels 7; Gaps 1;

Qy	187	TGAAGCTGGAATAAAGAGGGGTTTGCTGTGTAAAGGGGTTCAAGTACTACTGA	246
Db	31	TGAAGGCTGGAACCAAGACGGGGCTCTGTGTGTGAAGAGGGGTTCAAGTGTCTGTGA	90
Qy	247	CCACCATCGGCGCCTTTCGGCGCTTTTGCCCTCATGACCATCGCCATAGCACTGACTACT	306
Db	91	CGACGGTGGGGCCCTTTCGGCGCCTTCGACCCTCATGACCATCGCCATAGCACTGACTACT	150
Qy	307	GGCTCTACACAAAGAGCTCTCATCTGTGCAACACACCAACCTTACAGC-----AGTGAT	359
Db	151	GGCTCTACACGGCGCGCCTCTCATCTGTGCAACACCAACCTTACAGGCCCGCGCGAGAGAC	210
Qy	360	GACGACACACCCCATCGTGGGGCAGTGGCTCTTCGAGAAAGAGACCTTGGGGGCTTC	419

Db 211 GGGAGCCCTCCAGCTGGCGGGGCTGCGCGCCCTCGAGAGAGAGACCCCGCGGCTTC 270  
OY 420 ACACATTCAGGCTCTGGCGGATATGTCCTGGAAG 457  
Db 271 ACGCACTCGGCGCTCTGGAGAGATCTGCTGCTGGAAG 308

RESULT 2  
US-10-114-270-1  
; Sequence 1, Application US/10114270  
; Publication No. US20040030110A1  
; GENERAL INFORMATION:  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Malpankar, Uriel M.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Paturajan, Weera  
; APPLICANT: Liu, Ziaohong  
; APPLICANT: Gusev, Vladimir Y.  
; APPLICANT: Li, Li  
; APPLICANT: Verneet, Corine  
; APPLICANT: Zernusen, Bryan D.  
; APPLICANT: Gorman, Linda  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Pena, Carol E.A.  
; APPLICANT: Smithson, Glenda  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Shinkels, Richard A.  
; APPLICANT: Gangoli, Esha A.  
; APPLICANT: Taupier Jr., Raymond J.  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Ji, Weizhen  
; APPLICANT: Anderson, David W.  
; APPLICANT: Liete, Mario W.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Stone, David J.  
; APPLICANT: MacDougall, John R.  
; APPLICANT: Rothenberg, Mark E.  
; TITLE OF INVENTION: No. US20040030110A1 Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-322C  
; CURRENT APPLICATION NUMBER: US/10/114,270  
; CURRENT FILING DATE: 2002-11-27  
; PRIOR APPLICATION NUMBER: 60/281,086  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/281,136  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/281,863  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/281,906  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/282,020  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/282,930  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/282,934  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/283,512  
; PRIOR FILING DATE: 2001-04-12  
; PRIOR APPLICATION NUMBER: 60/283,710  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/284,234  
; PRIOR FILING DATE: 2001-04-17  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 470  
; SEQ ID NO 1  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:

; NAME/KEY: CDS  
; LOCATION: (55) .. (1024)  
US-10-114-270-1  
Query Match 14.7%; Score 96.4; DB 13; Length 1173;  
Best Local Similarity 83.8%; Pred. No. 7.7e-19;  
Matches 109; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

OY 187 TGAACGCTGGAAGAGAGAGGCTTGTGTGTAAGAGGCGCTTCAGGTACTACTGA 246  
DB 38 TGAACGCTGGAAGAGAGATGCGGGCCCTCTGTGTCGAGAGAGGGGTGAGGTGCTGCTGA 97  
OY 247 CCACATCGGCGGCTTGGCGGCTTTGGCTCATGACCATCGCATCGACTACT 306  
DB 98 CGACGATGCGGCGCTTGGCGGCTTGGCTCATGACCATCGCATCGACTACT 157  
OY 307 GCGTCTACAC 316  
DB 158 GCGTCTACAC 167

RESULT 3  
US-10-403-161-27  
; Sequence 27, Application US/10403161  
; Publication No. US20040043930A1  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, David et al.  
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 21402-573C  
; CURRENT APPLICATION NUMBER: US/10/403,161  
; CURRENT FILING DATE: 2003-03-31  
; PRIOR APPLICATION NUMBER: 60/370349  
; PRIOR FILING DATE: 2002-04-05  
; PRIOR APPLICATION NUMBER: 60/384543  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: 60/370969  
; PRIOR FILING DATE: 2002-04-08  
; PRIOR APPLICATION NUMBER: 60/403748  
; PRIOR FILING DATE: 2002-08-15  
; PRIOR APPLICATION NUMBER: 60/372019  
; PRIOR FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: 60/374379  
; PRIOR FILING DATE: 2002-04-22  
; PRIOR APPLICATION NUMBER: 09/779679  
; PRIOR FILING DATE: 2001-02-08  
; PRIOR APPLICATION NUMBER: 60/181045  
; PRIOR FILING DATE: 2000-02-08  
; PRIOR APPLICATION NUMBER: 10/055877  
; PRIOR FILING DATE: 2002-01-22  
; PRIOR APPLICATION NUMBER: 60/262892  
; PRIOR FILING DATE: 2001-01-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 173  
; SOFTWARE: Cnaseqdist version 0.1  
; SEQ ID NO 27  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (55) .. (1023)  
US-10-403-161-27  
Query Match 14.7%; Score 96.4; DB 13; Length 1173;  
Best Local Similarity 83.8%; Pred. No. 7.7e-19;  
Matches 109; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

OY 187 TGAACGCTGGAAGAGAGAGGCTTGTGTGTAAGAGGCGCTTCAGGTACTACTGA 246  
DB 38 TGAACGCTGGAAGAGATGCGGGCCCTCTGTGTCGAGAGAGGGGTGAGGTGCTGCTGA 97  
OY 247 CCACATCGGCGGCTTGGCGGCTTTGGCTCATGACCATCGCATCGACTACT 306



Db 98 CGACGGTGGGCGCTTCGGCGCTTCATGACCATCGCATAGACTACT 157  
Qy 307 GGGCTTACAC 316  
Db 158 GGGCTTACAC 167

RESULT 4  
US-09-883-483-1

; Sequence 1, Application US/09883483  
; Patent No. US20020128454A1  
; GENERAL INFORMATION:  
; APPLICANT: DUCKWORTH, David Malcolm  
; APPLICANT: HAYES, Philip David  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP-30180-D1  
; CURRENT APPLICATION NUMBER: US/09/883,483  
; CURRENT FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: UK 9819592.8  
; PRIOR FILING DATE: 1998-09-08  
; PRIOR APPLICATION NUMBER: 09/392,014  
; PRIOR FILING DATE: 1999-09-08  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 984  
; TYPE: DNA  
; ORGANISM: HOMO SAPIENS  
US-09-883-483-1

Query Match 13.2%; Score 86.4; DB 9; Length 984;  
Best Local Similarity 66.8%; Pred. No. 8e-16; Indels 0; Gaps 0;  
Matches 123; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

Qy 214 TGTGTGTGAAAAAGGCGCTTCAGTACTACTGACCAACATCGCGCTTCGCGGCTTTTG 273  
Db 5 TCGGATGCGACCGCGGCTGCGATGCTGCTGACCAAGCGGAGCTTCGCGGCTTCCT 64  
Qy 274 GCGTCTAGACCATCGGCATTCAGCATGCTACTGCTTACACAAAGCTTATCTGCA 333  
Db 65 CCTCATGCGCATCGGCATTCGCGACCGACTACTGCTGTAATCCACGCGGCACATCTGCA 124  
Qy 334 ACACCCGCAACCTCAGCAGGATGATGAGGACCCATCGTGGGGGAGTGGCTCT 393  
Db 125 AGGCGACCAACTGACCATGAGCAGCGGCCCCCGCGCGCGCGGAGCTCA 184  
Qy 394 CCGA 397  
Db 185 CCGA 188

RESULT 5  
US-10-276-774-825

; Sequence 825, Application US/10276774  
; Publication No. US20040053245A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; APPLICANT: Tang, Y, Tom et al  
; TITLE OF INVENTION: NO. US20040053245A1 Nucleic Acids and Polypeptides  
; FILE REFERENCE: 21272-030  
; CURRENT APPLICATION NUMBER: US/10/276,774  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 09/560,875  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: 09/496,914  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 2700  
; SOFTWARE: Custom  
; SEQ ID NO 825  
; LENGTH: 1252  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-276-774-825

Query Match 8.3%; Score 54.4; DB 13; Length 1252;  
Best Local Similarity 70.2%; Pred. No. 4.7e-06; Indels 0; Gaps 0;  
Matches 73; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 218 GTGTGAAAAGGCGCTTCAGTACTACTGACCAACATCGCGCTTCGCGGCTTTTG 277  
Db 291 GTTTGATCGAGGTGTTCAAAATGCTTTTACACACCGTGGTGGCTTCGCTTCAGCT 350  
Qy 278 CATGACCATCGGCATGACGATGCTACTGCTTACACAAAG 321  
Db 351 GATGACCATGCTGTGGGAACGACTATTGCTTACTACAG 394

RESULT 6  
US-10-276-774-780

; Sequence 780, Application US/10276774  
; Publication No. US20040053245A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; APPLICANT: Tang, Y, Tom et al  
; TITLE OF INVENTION: NO. US20040053245A1 Nucleic Acids and Polypeptides  
; FILE REFERENCE: 21272-030  
; CURRENT APPLICATION NUMBER: US/10/276,774  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 09/560,875  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: 09/496,914  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 2700  
; SOFTWARE: Custom  
; SEQ ID NO 780  
; LENGTH: 1383  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-276-774-780

Query Match 7.9%; Score 52; DB 13; Length 1383;  
Best Local Similarity 65.5%; Pred. No. 2.6e-05; Indels 0; Gaps 0;  
Matches 76; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Qy 218 GTGTGAAAAGGCGCTTCAGTACTACTGACCAACATCGCGCTTCGCGGCTTTTG 277  
Db 429 GTGTGACAGAGGTATCAATGTTATCACCAGTGAAGGCTTGGCTTTAGTT 488  
Qy 278 CATGACCATCGGCATGACGATGCTACTGCTTACACAAAGCTTATCTGCA 333  
Db 489 AATGACCATTTGCGAGCGGACGACTACTGTTATTCAGAGGTGTGACAGA 544

RESULT 7  
US-10-184-644-202/c

; Sequence 202, Application US/10184644  
; Publication No. US20030044930A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C227  
; CURRENT APPLICATION NUMBER: US/10/184,644  
; CURRENT FILING DATE: 2002-06-28  
; Prior Application removed - See file Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612





QY 8 TCACTTGACCTTGAGCTTGACGACCACTGCTGCTGCCCCGAGCCCCCTTGAGCCC 67  
DB 440 TCTCTGCGCCCCCCCCCCCCCTCCCGCGCGCCCCCCCCCCCCCCCCCCCCCCCC 381  
QY 68 TTGAGGCCCCCAGCTTGTGCTGTGTATCCCCCAGCGCGCGAGCCCCCCCC 127  
DB 380 CTCGCCCTCTCCCCCTCTCTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 321  
QY 128 TCCGCTGCGCGGCTGAGGCGGAGGCGCGCGGCTTGGC 166  
DB 320 CTTCTCTCCCGCGGCTCAACCCCGCCCCCTGCGCCCC 282

RESULT 14  
US-10-240-425-721/c

/ Sequence 721, Application US/10240425  
/ Publication No. US20040033502A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Williams, Amanda  
/ APPLICANT: Boland, Joseph P.  
/ APPLICANT: Lord, Reginald V.  
/ APPLICANT: Alvarez, Chris  
/ APPLICANT: Wetzel, Jon C.  
/ APPLICANT: Scheer, Uwe  
/ APPLICANT: Vockley, Joseph G.  
/ TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue  
/ FILE REFERENCE: 44921-5026  
/ CURRENT APPLICATION NUMBER: US/10/240,425  
/ PRIOR FILING DATE: 2002-09-30  
/ PRIOR APPLICATION NUMBER: PCT/US01/09847  
/ PRIOR FILING DATE: 2001-03-28  
/ PRIOR APPLICATION NUMBER: US 60/193,446  
/ PRIOR FILING DATE: 2000-03-31  
/ NUMBER OF SEQ ID NOS: 1588  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 721  
/ LENGTH: 451  
/ TYPE: DNA  
/ ORGANISM: Homo sapiens  
/ FEATURE:  
/ OTHER INFORMATION: Genbank Accession No. US20040033502A1 A1640222  
/ FEATURE:  
/ NAME/KEY: unsure  
/ LOCATION: (1)..(451)  
/ OTHER INFORMATION: n = a or c or g or t  
US-10-240-425-721

Query Match 6.6%; Score 43.6; DB 13; Length 451;  
Best Local Similarity 49.4%; Pred. No. 0.0065;  
Matches 76; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY 6 CTTGACTTGACCTTGAGCTTGACGACCACTGCTGCTGCCCCGAGCCCCCTTGAGCC 65  
DB 418 CCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 359  
QY 66 CTTGAGGCCCCCAGCTTGTGCTGTGTATCCCCCAGCGCGAGCGAGCCCCCG 125  
DB 358 CCCCCNNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 299  
QY 126 CTTGCTGCGCGGCTGAGGCGGAGGCGGCGGCTTGGC 159  
DB 298 CCCCCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 265

RESULT 15  
US-10-087-192-1942/c

/ Sequence 1942, Application US/10087192  
/ Publication No. US20020182586A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Morris, David W.  
/ APPLICANT: Engelhard, Eric K.  
/ TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR  
/ CANCER

/ FILE REFERENCE: 529452000122  
/ CURRENT APPLICATION NUMBER: US/10/087,192  
/ CURRENT FILING DATE: 2002-03-01  
/ PRIOR APPLICATION NUMBER: US 09/747,377  
/ PRIOR FILING DATE: 2000-12-22  
/ PRIOR APPLICATION NUMBER: US 09/798,586  
/ PRIOR FILING DATE: 2001-03-02  
/ NUMBER OF SEQ ID NOS: 2059  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 1942  
/ LENGTH: 71292  
/ TYPE: DNA  
/ ORGANISM: Homo sapiens  
US-10-087-192-1942

Query Match 6.6%; Score 43.2; DB 13; Length 71292;  
Best Local Similarity 55.3%; Pred. No. 0.046;  
Matches 84; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 15 GCACCTTGACCTTGAGCACTGCTGCTGCCCCGAGCCCCCTTGAGAGC 74  
DB 9654 GCGGCTCGGCGGAGACGCTTCACTCCCCCGCGCGCGCGCGCGCGCGCGCG 9595  
QY 75 CCCCCAGCTTGTGCTGTGTATCCCCCAGCGCGGCGGCGCGCGCGCGCGCGCG 134  
DB 9594 CCGCTGCGCTGCG 9535  
QY 135 CCGGCTGAGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 166  
DB 9534 CTTGAGGAGCG 9503

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Job time : 314 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2004, 15:34:27 ; Search time 66 Seconds

(without alignments)  
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Title: US-10-060-066-2

Perfect score: 656  
Sequence: 1 tatgcttaccctgcacct.....tgctattttttcttcttg 656

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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3: /cgn2\_6/prodata/2/ina/6A\_COMB.seq:\*  
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5: /cgn2\_6/prodata/2/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/prodata/2/ina/backfillseq1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86.4	13.2	984	3 US-09-392-014-1	Sequence 1, Appl
2	83.2	12.7	1071	4 US-09-123-030-11	Sequence 11, Appl
3	53.6	8.2	1477	4 US-09-123-030-9	Sequence 9, Appl
4	52.8	8.0	1558	4 US-09-123-030-7	Sequence 7, Appl
5	45.8	7.0	4403765	3 US-09-103-840A-2	Sequence 2, Appl
6	45.8	7.0	4411529	3 US-09-103-840A-1	Sequence 1, Appl
7	42.8	6.5	1926	4 US-09-249-585A-2	Sequence 2, Appl
8	42.8	6.5	1926	4 US-09-410-399-3	Sequence 3, Appl
9	42.8	6.5	2580	4 US-09-050-863-2	Sequence 2, Appl
10	42.8	6.5	2580	4 US-09-359-081-2	Sequence 2, Appl
11	42.8	6.5	5452	2 US-09-130-114-1	Sequence 1, Appl
12	42.8	6.5	8705	4 US-09-647-344A-14	Sequence 14, Appl
13	42.8	6.5	9600	4 US-08-910-647-1	Sequence 1, Appl
14	42.8	6.5	10596	1 US-07-884-811-15	Sequence 15, Appl
15	42.8	6.5	10596	1 US-07-885-971-15	Sequence 15, Appl
16	42.8	6.5	10596	1 US-08-087-783A-15	Sequence 15, Appl
17	42.8	6.5	10596	1 US-08-087-783A-15	Sequence 15, Appl
18	42.8	6.5	10596	1 US-08-194-088B-15	Sequence 15, Appl
19	42.8	6.5	10596	5 PCT-US93-04648-15	Sequence 15, Appl
20	42.8	6.5	10596	5 PCT-US93-04648-15	Sequence 15, Appl
21	42.8	6.5	16080	4 US-09-724-566A-48	Sequence 48, Appl
22	41.4	6.3	4403765	3 US-09-103-840A-2	Sequence 2, Appl
23	41.4	6.3	4411529	3 US-09-103-840A-1	Sequence 1, Appl
24	41.2	6.3	320	3 US-09-165-264-7	Sequence 7, Appl
25	39.8	6.1	1347	3 US-09-140-804-1	Sequence 1, Appl
26	39.8	6.1	1347	4 US-09-686-838B-1	Sequence 1, Appl
27	39.8	6.1	1377	4 US-09-866-028-41	Sequence 41, Appl

c 28	39.6	6.0	320	3 US-09-165-264-11	Sequence 11, Appl
c 29	39.6	6.0	1382	4 US-09-016-434-1256	Sequence 1256, Ap
c 30	39.6	6.0	152331	3 US-09-128-155-16	Sequence 16, Appl
c 31	39.4	6.0	4257	2 US-08-690-473-1	Sequence 1, Appl
c 32	39.4	6.0	4257	3 US-08-259-821A-1	Sequence 1, Appl
c 33	39.4	6.0	4257	3 US-08-843-659-1	Sequence 1, Appl
c 34	39.4	6.0	12001	1 US-08-458-568A-11	Sequence 11, Appl
c 35	38.2	5.8	319	3 US-09-165-264-8	Sequence 8, Appl
c 36	38.2	5.8	320	3 US-09-165-264-14	Sequence 14, Appl
c 37	38	5.8	7218	1 US-08-232-463-14	Sequence 14, Appl
c 38	37.8	5.8	318	3 US-09-165-264-12	Sequence 12, Appl
c 39	37.8	5.8	320	3 US-09-165-264-13	Sequence 13, Appl
c 40	37.6	5.7	12001	1 US-08-458-568A-11	Sequence 11, Appl
c 41	37.4	5.7	364	4 US-09-621-976-17202	Sequence 17202, A
c 42	37.2	5.7	1062	4 US-09-016-434-1286	Sequence 1286, Ap
c 43	37.2	5.7	1062	4 US-08-134-231C-33	Sequence 33, Appl
c 44	37.2	5.7	1062	4 US-09-023-655-1327	Sequence 1327, Ap
c 45	37.2	5.7	1062	4 US-08-728-160-33	Sequence 33, Appl

## ALIGNMENTS

RESULT 1	US-09-392-014-1	Application US/09392014
Sequence 1, Appl	Patent No. 6274380	GENERAL INFORMATION:
APPLICANT: David Malcolm Duckworth	APPLICANT: Philip David Hayes	TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30180	CURRENT APPLICATION NUMBER: US/09/392,014	CURRENT FILING DATE: 1999-09-08
EARLIER APPLICATION NUMBER: UK 9819592.8	EARLIER FILING DATE: 1998-09-08	NUMBER OF SEQ ID NOS: 4
SOFTWARE: FaastSeq for Windows Version 3.0	SEQ ID NO 1	LENGTH: 984
TYPE: DNA	ORGANISM: HOMO SAPIENS	US-09-392-014-1
Query Match	13.2%;	Score 86.4; DB 3; Length 984;
Best Local Similarity	66.8%;	Pred. No. 5.5e-14;
Matches 123; Conservative	0; Mismatches 61;	Indels 0; Gaps 0;
QY	214 TGTGATGCAAAAGGCGTTCAGGTA	CTGACCAACATCGGCGCTTTCGGGCTTTTG 273
DB	5 TGGATGCAACCGCGGCTGCAATCTCTGACCA	CGGCGGAGCTTTCGGGCTTCT 64
QY	274 GCGTCATGACATCGGCATCAGCATGTA	CTGACTGCTCTACACAAGGCTTCATCTGCA 333
DB	65 CGGTATGCAATCGCATCGGACGACGATTA	CTGCTGTAATCAAGCGGACATCTGCA 124
QY	334 ACAACCACTACAGAGTGATGACGACCA	CCCATGTTGGGGGCACTGCTCT 393
DB	125 ACGGCACTCACTGACATGACGACGAGG	CGGCGGCGGCGGCGGACCTCA 184
QY	394 CCGA 397	
DB	185 CCGA 188	
RESULT 2	US-09-123-030-11	Application US/09123030
Sequence 11, Appl	Patent No. 6365337	GENERAL INFORMATION:
APPLICANT: Letts, Verity A.	APPLICANT: Frankel, Wayne N.	APPLICANT: Campbell, Kevin P.

```
/ APPLICANT: Felix, Ricardo
/ TITLE OF INVENTION: Genes Encoding Neuronal Voltage-gated Calcium Channel
/ TITLE OF INVENTION: Gamma Subunits
/ FILE REFERENCE: US App. 09/123,030
/ CURRENT APPLICATION NUMBER: US/09/123,030
/ CURRENT FILING DATE: 1998-07-27
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 11
/ LENGTH: 1071
/ TYPE: DNA
/ ORGANISM: Murinae gen. sp.
/ FEATURE:
/ NAME/KEY: 5'UTR
/ LOCATION: (1)..(121)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (22)..(1002)
/ FEATURE:
/ NAME/KEY: 3'UTR
/ LOCATION: (1003)..(1071)
/ US-09-123-030-11
```

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Query Match      12.7%; Score 83.2; DB 4; Length 1071;
Best Local Similarity 65.8%; Pred. No. 4,1e-13;
Matches 121; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
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```
QY 214 TGTGTGTAAGGCGCTTCAGGTACTAGTACCAACCATCGGCGCTTTG 273
DB 26 TGGCATGCGACCGCGGCTGAGATGCTCTGACCAAGCGGCGGCGCTTCT 85
QY 274 GCGTATGACATCGCATGACACTGACTGCTGCTACAGAGCTTCATCTGA 333
DB 86 CGCTATGCGCATCGCATGCGACCGACTACCGGCTGATCTCAGCGCATCTGCA 145
QY 334 ACACCAACCACTCAGACGAGGTATGACGACCAACCCCATGCGGCGAGTGCCTCT 393
DB 146 ACGGACCAACTGATGACATGACGACGAGGCGGCGGCGGCGGCGGCGGCGACTCA 205
QY 394 CCGA 397
DB 206 CCGA 209
```

```
RESULT 3
US-09-123-030-9
/ Sequence 9, Application US/09123030
/ Patent No. 6365337
```

```
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Letts, Verily A.
/ APPLICANT: Frankel, Wayne N.
/ APPLICANT: Campbell, Kevin P.
/ APPLICANT: Felix, Ricardo
/ APPLICANT: Biddlecome, Gloria
/ TITLE OF INVENTION: Genes Encoding Neuronal Voltage-gated Calcium Channel
/ FILE REFERENCE: US App. 09/123,030
/ CURRENT APPLICATION NUMBER: US/09/123,030
/ CURRENT FILING DATE: 1998-07-27
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 9
/ LENGTH: 1477
/ TYPE: DNA
/ ORGANISM: Murinae gen. sp.
/ FEATURE:
/ NAME/KEY: 5'UTR
/ LOCATION: (1)..(487)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (488)..(1432)
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```
/ FEATURE:
/ NAME/KEY: 3'UTR
/ LOCATION: (1433)..(1477)
/ US-09-123-030-9
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Query Match      8.2%; Score 53.6; DB 4; Length 1477;
Best Local Similarity 66.4%; Pred. No. 4,6e-05;
Matches 77; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
```

```
QY 218 GTGTGTAAGGCGCTTCAGTACTAGTACCAACCATCGGCGCTTTG 277
DB 496 GTGTACAGAGTATCCAGATGTGATCCTACTGTAGAGCCCTTGGAGCTTTAGTTT 555
QY 278 CATGACCATCGCATGACACTGACTGCTCTACAGAGCTTCATCTGCA 333
DB 556 AATGACATTGCAATGGGCAAGGACTGCTATTTCCAGAGTGTGTGAGGA 611
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```
RESULT 4
US-09-123-030-7
/ Sequence 7, Application US/09123030
/ Patent No. 6365337
```

```
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Letts, Verily A.
/ APPLICANT: Frankel, Wayne N.
/ APPLICANT: Campbell, Kevin P.
/ APPLICANT: Felix, Ricardo
/ APPLICANT: Biddlecome, Gloria
/ TITLE OF INVENTION: Genes Encoding Neuronal Voltage-gated Calcium Channel
/ FILE REFERENCE: US App. 09/123,030
/ CURRENT APPLICATION NUMBER: US/09/123,030
/ CURRENT FILING DATE: 1998-07-27
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 7
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/ LENGTH: 1558
/ TYPE: DNA
/ ORGANISM: Murinae gen. sp.
/ FEATURE:
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/ NAME/KEY: 5'UTR
/ LOCATION: (1)..(389)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (390)..(1361)
/ FEATURE:
/ NAME/KEY: 3'UTR
/ LOCATION: (1361)..(1558)
/ US-09-123-030-7
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Query Match      8.0%; Score 52.8; DB 4; Length 1558;
Best Local Similarity 69.2%; Pred. No. 7,7e-05;
Matches 72; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
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```
QY 218 GTGTGTAAGGCGCTTCAGTACTAGTACCAACCATCGGCGCTTTG 277
DB 398 GTTGTATGAGAGTGTTCAAATGCTTTTAAACCAAGCTTTCGCTTCAGCTT 457
QY 278 CATGACCATCGCATGACACTGACTGCTTCATCAAGAG 321
DB 458 GATGACCATCGCTGTGGGAACCGACTATTGCTGTACTCCAGAG 501
```

```
RESULT 5
US-09-103-840A-2
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```
/ Sequence 2, Application US/09103840A
/ Patent No. 6294328
```

```
/ GENERAL INFORMATION:
```

```
/ APPLICANT: FLEISCHMAN, Robert D.
/ APPLICANT: WHITE, Owen R.
/ APPLICANT: FRASER, Claire M.
/ APPLICANT: VENTER, John C.
```







ORGANISM: VEBNA  
US-09-130-114-1

Query Match 6.5%; Score 42.8; DB 2; Length 5452;  
Best Local Similarity 58.7%; Pred. No. 0.062;  
Matches 74; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 13 CTGCACCTTGGCTGAGACCACTGCTGCGCCCGGCGCCCTGAGCCCTTGGAG 72

DB 1440 CTCACCTCTGCTGCTGCGCCCTGCTGCTGCGCCCTGCTGCTGCTGCTGCTG 1499

QY 73 GCGCCCACTTCTGCTGCTGCTGATCCCCCAAGCCGCGACAGCGCCGCTCCG 132

DB 1500 CCCCTCTGCTGCTGCGCCCTGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 1559

QY 133 TGCCCC 138  
DB 1560 CTGCCC 1565

## RESULT 12

US-09-647-344A-14  
Sequence 14, Application US/09647344A

Patent No. 6586180

GENERAL INFORMATION:

APPLICANT: Ruffner, Duane B.

APPLICANT: Pierce, Michael L.

APPLICANT: Chen, Zhidong

TITLE OF INVENTION: Directed Antisense Libraries

FILE REFERENCE: T6678.PCT.US

CURRENT APPLICATION NUMBER: US/09/647,344A

PRIOR APPLICATION NUMBER: PCT/US99/06742

PRIOR FILING DATE: 1999-03-28

NUMBER OF SEQ ID NOS: 50

SEQ ID NO 14

LENGTH: 8705

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: pshuttle

US-09-647-344A-14

Query Match 6.5%; Score 42.8; DB 4; Length 8705;  
Best Local Similarity 58.7%; Pred. No. 0.074;  
Matches 74; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 13 CTGCACCTTGGCTGAGACCACTGCTGCGCCCGGCGCCCTTGGAG 72

DB 7305 CTCACCTCTGCTGCTGCGCCCTGCTGCTGCGCCCTGCTGCTGCTGCTGCTG 7364

QY 73 GCGCCCACTTCTGCTGCTGCTGATCCCCCAAGCCGCGACAGCGCCGCTCCG 132

DB 7365 CCCCTCTGCTGCTGCGCCCTGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 7424

QY 133 TGCCCC 138  
DB 7425 CTGCCC 7430

## RESULT 13

US-08-910-647-1/C  
Sequence 1, Application US/08910647

Patent No. 6251433

GENERAL INFORMATION:

APPLICANT: Zuckermann et al.

TITLE OF INVENTION: Compositions and Methods for

TITLE OF INVENTION: Polynucleotide Delivery

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESS: Chiron Corporation

STREET: 4560 Horton Street

CITY: Emeryville

STATE: California

COUNTRY: U.S.A.

ZIP: 94608-2916

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/910,647

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Fujita, Sharon M.

REFERENCE/DOCKET NUMBER: 1218.002

TELEPHONE: (510) 923-2706

TELEFAX: (510) 655-3542

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 9600 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-910-647-1

Query Match 6.5%; Score 42.8; DB 3; Length 9600;  
Best Local Similarity 58.7%; Pred. No. 0.077;  
Matches 74; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 13 CTGCACCTTGGCTGAGACCACTGCTGCGCCCGGCGCCCTTGGAG 72

DB 1411 CTCACCTCTGCTGCTGCGCCCTGCTGCTGCGCCCTGCTGCTGCTGCTGCTG 1352

QY 73 GCGCCCACTTCTGCTGCTGCTGATCCCCCAAGCCGCGACAGCGCCGCTCCG 132

DB 1351 CCCCTCTGCTGCTGCGCCCTGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 1292

QY 133 TGCCCC 138  
DB 1291 CTGCCC 1286

## RESULT 14

US-09-620-925-1/C  
Sequence 1, Application US/09620925

Patent No. 6468986

GENERAL INFORMATION:

APPLICANT: Zuckermann et al.

TITLE OF INVENTION: Compositions and Methods for

TITLE OF INVENTION: Polynucleotide Delivery

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESS: Chiron Corporation

STREET: 4560 Horton Street

CITY: Emeryville

STATE: California

COUNTRY: U.S.A.

ZIP: 94608-2916

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/620,925

FILING DATE: 21-Jul-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/910,647

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
 NAME: Fujita, Sharon M.  
 REGISTRATION NUMBER: 38,459  
 REFERENCE/DOCKET NUMBER: 1219.002  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (510) 923-2706  
 TELEFAX: (510) 655-3542  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9600 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 US-09-620-925-1

Query Match	6.5%	Score	42.8	DB	4	length	9600
Best Local Similarity	58.7%	Pred.	No.	0.077			
Matches	74	Conservative	0	Mismatches	52	Indels	0
						Gaps	0

[illegible]

RESULT 15  
US-07-884-811-15/c  
; Sequence 15, Application US/07884811

; Patent No. 5316921

GENERAL INFORMATION:

TITLE OF INVENTION: SINGLE-CHAIN HERATOCYTE GROWTH FACTOR VARIANTS

NUMBER OF SEQUENCES:	21
----------------------	----

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San F

STATE: Calif  
COUNTY: LOS ANGELES

COUNTRY: USA  
ZTD: 94090

211: 34080  
 212: COMPUTER READAB

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (Genentech)

```
; CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/01/884,811  
FILING DATE: 19930518

FILED DATE: 199203-  
CLASSIFICATION: 530

PRIOR APPLICATION DATA

APPLICATION NUMBER:

**FILING DATE:**

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Ginger R.

REGISTRATION NUMBER: 33,055

REFERENCE/DOCUMENT NUMBER: 755.1  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-3216

TELEFAX: 415/952-98

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 15:

### SEQUENCE CHARACTERISTICS:

LENGTH: 10596 bases

TYPE: NUCLEIC ACID

```

; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-084-811-15

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Query Match	6.5%	Score 42.8;	DB 1;	Length 10596;
Best Local Similarity	58.7%;	Pred. No. 0.08;		
Matches 74; Conservative	0;	Mismatches 52;	Indels 0;	Gaps 0;

QY 13 TTGACACCTGGCCCTCTGAGAGCAGACTGGTGGCTGCCCCGGGACCCCTTGAGCCCTTGAG 72

Db 2945 CTCACACTCTGCTCTCTGCTGCCCCCTCTGCTCTGCCCCCTCTCTGCTCTGCCCCCTCTG 2886

QY 73 GCCCCCAAGCTTCTGCTGCTGCTGTGATCCCCCAAGCCGCGAGCAGGACCCGCGCTCGGC 132

Db 2885 CCCCCTCTGCTCTGCCCCCTCTGCCCCCTCTGACTCTGCCCCCTCTGCCCCCTCTGACTC 2822

QY 133 TGCCCC 138

Db 2825 CTGCCC 2820

Search completed: May 22, 2004, 17:00:50  
Job time : 83 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using bw model

Run on: May 22, 2004, 14:52:52 ; Search time 2049 Seconds

(without alignments)  
13876.540 Million cell updates/sec

Title: US-10-060-066-2

Perfect score: 656

Sequence: 1 tatggcttcacctgcacact.....tggtattttattcttcttcttg 656

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Genemdb1:\*  
1: gb\_ba:\*  
2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_seb:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_ov:\*  
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23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_seb:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_hcg\_hum:\*  
31: em\_hcg\_inv:\*  
32: em\_hcg\_ocher:\*  
33: em\_hcg\_mus:\*  
34: em\_hcg\_pin:\*  
35: em\_hcg\_rtd:\*  
36: em\_hcg\_mam:\*  
37: em\_hcg\_vrt:\*  
38: em\_sy:\*  
39: em\_hcgo\_hum:\*  
40: em\_hcgo\_mus:\*  
41: em\_hcgo\_ocher:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	592.8	90.4	185639	2	AC079557	AC079557 Mus muscu
C 2	519.4	79.2	244548	2	AC128446	AC128446 Rattus no
C 3	519.4	79.2	246624	2	AC114434	AC114434 Rattus no
4	387.4	59.1	1380	9	AF361350	AF361350 Mus muscu
5	297.8	45.4	169997	9	AC008440	AC008440 Homo sapi
6	269.8	41.1	1266	10	AF361346	AF361346 Rattus no
7	236	36.0	190210	2	AC022318	AC022318 Homo sapi
8	232.2	35.4	1386	9	AF361354	AF361354 Homo sapi
9	191.2	29.1	633	9	AF234892	AF234892 Homo sapi
10	171	26.1	1281	9	AF288388	AF288388 Homo sapi
11	92	14.0	987	5	AY037891	AY037891 Gallus ga
12	86.4	13.2	720	9	HSCACNG1	AF142622 Homo sapi
13	86.4	13.2	984	6	AR165149	AR165149 Sequence
14	86.4	13.2	984	6	AX101260	AX101260 Sequence
15	86.4	13.2	984	10	MMU272045	AJ272045 Mus muscu
16	86.4	13.2	984	10	AF361341	AF361341 Rattus no
17	86.4	13.2	1001	9	AF162692	AF162692 Homo sapi
18	86.4	13.2	3392	9	BC034532	BC034532 Homo sapi
19	86.4	13.2	94538	10	AL645853	AL645853 Mouse DNA
20	86.4	13.2	173126	9	AC005988	AC005988 Homo sapi
21	86.4	13.2	178380	2	AC129819	AC129819 Rattus no
22	83.2	12.7	1071	6	AR202726	AR202726 Sequence
23	75.4	11.5	209887	2	AC079424	AC079424 Mus muscu
24	62.4	9.5	1548	5	AF118819	AF118819 Gallus ga
25	61.4	9.4	3067	5	BC057439	BC057439 Danio rer
26	58.6	8.9	123020	5	AF429315	AF429315 Homo sapi
27	57.6	8.8	196036	5	BX004779	BX004779 Zebrafish
28	56.2	8.6	203225	5	BX255942	BX255942 Zebrafish
29	54.6	8.3	126667	2	AC015839	AC015839 Homo sapi
30	54.4	8.3	972	9	AF096332	AF096332 Homo sapi
31	54.4	8.3	70881	9	BX284660	BX284660 Human DNA
32	54.4	8.3	99497	9	HS29316	AL049749 Human DNA
33	53.6	8.2	948	10	MMU272044	AJ272044 Mus muscu
34	53.6	8.2	948	10	AF361340	AF361340 Rattus no
35	53.6	8.2	1477	6	AR202725	AR202725 Sequence
36	53.6	8.2	191935	10	AC016522	AC016522 Mus muscu
37	53.6	8.2	237373	2	AC094178	AC094178 Rattus no
38	53.6	8.2	252720	2	AC132248	AC132248 Mus muscu
39	53.2	8.1	63082	2	AC022663	AC022663 Homo sapi
40	52.8	8.0	972	10	AF361339	AF361339 Rattus no
41	52.8	8.0	1124	10	AF118818	AF118818 Rattus no
42	52.8	8.0	1554	10	AF077739	AF077739 Mus muscu
43	52.8	8.0	1558	6	AR202724	AR202724 Sequence
44	52.8	8.0	197660	10	AL589650	AL589650 Mouse DNA
45	52.8	8.0	208651	10	AC090493	AC090493 Genomic s

#### ALIGNMENTS

RESULT 1  
AC079557/c 185839 bp DNA 1linear HTG 02-SBP-2000  
LOCUS  
DEFINITION Mus musculus clone RP23-449P12, WORKING DRAFT SEQUENCE, 16  
unoriented pieces.  
ACCESSION AC079557  
VERSION AC079557.1 GI:9964922  
KEYWORDS HTG, HTGS PHASE1, HTGS DRAFT.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS 1 (bases 1 to 185839)  
TITLE DOE Joint Genome Institute.  
Sequencing of Mouse

JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 185839)  
AUTHORS DOE Joint Genome Institute.  
TITLE Direct Submission  
JOURNAL Submitted (02-SEP-2000) Production Sequencing Facility, DOE Joint  
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
-----Genome Center  
Center: Joint Genome Institute  
Center Code: JGI  
Web site: <http://www.jgi.doe.gov>

-----  
Project Information  
Center Project Name: 1909420  
Center clone name: RPCI-23\_449F12  
-----

Summary Statistics  
Consensus quality: 172503 bases at least Q40  
Consensus quality: 17768 bases at least Q30  
Consensus quality: 179073 bases at least Q20  
Estimated insert size: 187000; agarose-fp estimation  
Estimated insert size: 184339; sum-of-coverage estimation  
Quality coverage: 7.81 in Q20 bases; agarose-fp estimation  
Quality coverage: 7.93 in Q20 bases; sum-of-coverage estimation.  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 16 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 1081: contig of 1081 bp in length  
\* 1082 1181: gap of unknown length  
\* 1182 4298: contig of 3117 bp in length  
\* 4299 4398: gap of unknown length  
\* 4399 6732: contig of 2334 bp in length  
\* 6733 6832: gap of unknown length  
\* 6833 11626: contig of 4794 bp in length  
\* 11627 11726: gap of unknown length  
\* 11727 15545: contig of 3819 bp in length  
\* 15546 15645: gap of unknown length  
\* 15646 20007: contig of 4362 bp in length  
\* 20008 20107: gap of unknown length  
\* 20108 26156: contig of 6049 bp in length  
\* 26157 32958: gap of unknown length  
\* 32959 33058: contig of 6702 bp in length  
\* 33059 42014: gap of unknown length  
\* 42015 42114: gap of 8956 bp in length  
\* 42115 50688: contig of 8574 bp in length  
\* 50689 50788: gap of unknown length  
\* 50789 61398: contig of 10510 bp in length  
\* 61399 61398: gap of unknown length  
\* 61399 77269: contig of 15871 bp in length  
\* 77270 77369: gap of unknown length  
\* 77370 95693: contig of 1824 bp in length  
\* 95694 95793: gap of unknown length  
\* 95794 119999: contig of 24206 bp in length  
\* 120000 120099: gap of unknown length  
\* 120100 150273: contig of 30174 bp in length  
\* 150274 150374: gap of unknown length  
\* 150374 185839: contig of 35466 bp in length.

## FEATURES

source  
1. 185839  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
/clone="RP23-449F12"  
/clone\_lib="RPCI mouse BAC library 23"

## ORIGIN

Query Match 90.4%; Score 592.8; DB 2; Length 185839;  
Best Local Similarity 95.3%; Pred. No. 26-129;

Matches 625; Conservative 0; Mismatches 29; Indels 2; Gaps 2;  
QY 1 TATGCTTCACCTGACCACTTGCCCTGACGACCACTGCTGCGCCCGCCCGCCCTC 60  
DB 57586 TATGCTTCACCTG-ACCTTCGCTCTGACAGCACTGCTGCTGCCCCCGCCCTC 57528  
QY 61 TGGCCCTTGAAGCCCGCCAGCTTCTGCTGCTGCTGATCCCGCCAGCCGCGACGG 120  
DB 57527 TGGCCCTTGAAGCCCGCCAGCTTCTGCTGCTGCTGATCCCGCCAGCCGCGACGG 57468  
QY 121 CCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
DB 57467 CCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 57408  
QY 181 AGTCATTGAAAGCGCTGAATGAAGAGAGGCTTGTGTGTGTAAGAGGCGCTTCAGTAC 240  
DB 57407 AGTCATTGAAAGCGCTGAATGAAGAGAGGCTTGTGTGTGTAAGAGGCGCTTCAGTAC 57348  
QY 241 TACTGACCAACCATGCGCGCTTCGCGGCTTTTGGCTTCATGACCATGCGACCTG 300  
DB 57347 TACTGACCAACCATGCGCGCTTCGCGGCTTTTGGCTTCATGACCATGCGACCTG 57288  
QY 301 ACTACTGCTTACACAGAGCTCTCATCTGCAACACCACTCAGCAGGTATG 360  
DB 57287 ACTACTGCTTACACAGAGCTCTCATCTGCAACACCACTCAGCAGGTATG 57228  
QY 361 ACGGACCAACCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420  
DB 57227 ACGGACCAACCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 57168  
QY 421 CACATTCAGGCTCTGCGGATATGCTGCTGCAAGATGAGGTGACGAGAGCCCTGCT 480  
DB 57167 CACATTCAGGCTCTGCGGATATGCTGCTGCAAGATGAGGTGACGAGAGCCCTGCT 57108  
QY 481 GCGCACTCCGATGAGGCTTGTGCTTNCAGCAATTCAGCTTGTGAGTCTCA 540  
DB 57107 GCGCACTCCGATGAGGCTTGTGCTTNCAGCAATTCAGCTTGTGAGTCTCAT 57048  
QY 541 CCAGAGCTTGAAGGCTTGTGCTTGTGCTGAGAGGCGGATTCATGACACCCCTCA 600  
DB 57047 CCAGAGCTTGAAGGCTTGTGCTTGTGCTGAGAGGCGGATTCATGACACCCCTCA 56988  
QY 601 TNCCTTNTACAAATCCCTCTTCTGCGGATTTGATTTATTTATTTCTTGG 656  
DB 56987 TCCCTCTGT-CCAATCCCTCTTCTGCGGATTCGCTTATTTATTTATTTATCTG 56933  
RESULT 2  
AC128446/c 244548 bp DNA linear HTG 09-OCT-2002  
AC128446/c  
DEFINITION Rattus norvegicus clone CH230-95B19, \*\*\* SEQUENCING IN PROGRESS  
LOCUS \*\*\*  
ACCESSION AC128446  
VERSION AC128446.2 GI:22856047  
KEYWORDS HTG; PHASE2; HTGS; DRAFT; HTGS\_ENRICHED.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
REFERENCE 1 (bases 1 to 244548)  
Murray, D., Marie, M., Merker, M., Lee, A., Adams, S., Alder, J.,  
Allen, C., Allen, H., Albrooks, S., Amin, A., Anguiano, D.,  
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,  
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,  
Biswal, N., Blair, U., Blankenburg, K., Blyth, P., Brown, M.,  
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,  
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,  
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,  
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., P. Souza, L.,  
David, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dedetich, D.,  
Deigado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Diya, K.,  
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,



LOCUS	246624 bp	DNA	linear	HG 21-SEP-2002
DEFINITION	AC114434	246624 bp	DNA	linear
VERSION	AC114434.3	GI:23266184		
KEYWORDS	HTG; HTGS PHASE2; HTGS DRAFT; HTGS ENRICHED.			
SOURCE	Rattus norvegicus (Norway rat)			
ORGANISM	Rattus norvegicus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
AUTHORS	1 (bases 1 to 246624)			
	Muzy D,Marie, Metzker M, Lee, Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angiardo, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Barnstead, F., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Butrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Cesaar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Ande, C., Dedrich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Din, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Frazer, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Georgegeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamli, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlik, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Ididibit, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, Y., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensenheva, L., Louisseg, H., Lozdo, R. T., Lu, X., Ma, J., Maneshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangun, P., Mapua, P., Martin, K., Martin, R., Martinez, E., Mahaniny, S., McLeod, M. P., McNell, T. Z., Meenen, E., Milosavljevic, A., Miner, G., Minia, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidas, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwokilemeh, O., Okwomu, G., Olarinmaga, A., Pal, S., Parks, K., Paeternack, S., Paul, H., Perez, A., Perez, L., Pfankoch, C., Plopper, F., Poindexter, A., Popovic, D., Prims, E., Pu, L., Puzo, M., Quito, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R., Kelly, B., Rellly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rivers, C., Rodkey, T., Rojals, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sison, I., Sitter, C. D., Smaj, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Soosa, J., Stealm, M., Strong, R., Sutton, A., Svetek, A., Taber, P., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Umant, K., Valdes, R., Vetz, V., Villaseana, D., Walron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wiczek, R., Woden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, P., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Weidenhausen, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstock, G. and Gibbs, R. A.			
TITLE	Unpublished			
REFERENCE	2 (bases 1 to 246624)			
AUTHORS	Worley K. C.			
JOURNAL	Direct Submission			
TITLE	Submitted (09-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA			
REFERENCE	3 (bases 1 to 246624)			
AUTHORS	Rat Genome Sequencing Consortium.			
TITLE	Direct Submission			
JOURNAL	Submitted (21-SEP-2002) Human Genome Sequencing Center, Department			

of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Sep 21, 2002 this sequence version replaced gi:21737492. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/project/rat/>). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center -----

Center: Baylor College of Medicine

Center code: BCM

Web Site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information -----

Center project name: GPFX

Center clone name: CH230-210C18

----- Summary Statistics -----

Assembly program: Phrap; version 0.990329

Consensus quality: 214395 bases at least Q40

Consensus quality: 216765 bases at least Q30

Consensus quality: 218383 bases at least Q20

Estimated insert size: 238927; sum-of-contigs estimation

Quality coverage: 4x in Q20 bases; sum-of-contigs estimation

-----

\* NOTE: Estimated insert size may differ from sequence length (see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)).

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 1 contigs. Gaps between the contigs

\* are represented as runs of N. The order of the pieces

\* is believed to be correct as given, however the sizes

\* of the gaps between them are based on estimates that have

\* provided by the submittor.

\* This sequence will be replaced

\* by the finished sequence as soon as it is available and

\* the accession number will be preserved.

1 246624: contig of 246624 bp in length.

Location/Qualifiers

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/organism="Rattus norvegicus"

/mol\_type="genomic DNA"

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/clone="CH230-210C18"

144..702

/note="clone\_boundary"

clone end: T7

size: EcoRI

end\_sequence: BH344045"

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misc\_feature

complement(244274..244949)

/note="clone boundary"

clone end: Sp6

size: EcoRI

end\_sequence: BH344045"

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ORIGIN

Query Match 79.2%; Score 519.4; DB 2; Length 246624;

Best Local Similarity 94.0%; Pred. No. 4.4e-112;

Matches 568; Conservative 0; Mismatches 33; Indels 3; Gaps 3;

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174382 ATGACTTCACTCTG-ACCTCGGCTCTGTGACGCACTCTGCTGCTGCCCCCTT-CCCTCT 1743255

62 GGGCCCTTGAAGCCCCCGCAAGTTCTGCTGTGCTGTGATCCCCCAAGCCGCGGACCGG 121

174324 GGGCCCTGAGAGCCCCCGCAGCTTCTGCTGTGCTGTGACCCCCCAGCCGCGGACCGG 1742655

122 CCGGCTTCGCTGCGCCGGTGTGTGGCCACAGAGCCCCCGGTTGCGAGTGTGAAATGGA 181

174264 CCGGCTTCGCTGCGCCGGTGTGTGGCCACAGAGCCCCCGGTTGCGAGTGTGAAATGGA 1742055

182 GTCAATTGAACGCTGGAATGAGAGAGGGGTTTGTGTGTGTGAAAAAGGCGTTCAAGTACT 241



Db 174204 ATCATGAAACGCTGGAATGAAGAGGGGTTGTGTGCGAAGAGGGGCTTCAAGTACT 174145  
Qy 242 ACTGACACCATGAGGGGCTTCCGGCTTTTGCTTCATATACCATGCTTACGACTGA 301  
Db 174144 ACTGACACCATGAGGGGCTTCCGGCTTTTGCTTCATATACCATGCTTACGACTGA 174085  
Qy 302 CTACAGGCTCTACAGAGAGCTCTCATCTGCAACACACCACTTCAAGCAGGTATGA 361  
Db 174084 CTACAGGCTCTACAGAGAGCTCTCATCTGCAACACACCACTTCAAGCAGGTATGA 174025  
Qy 362 CGGACACACCATGAGGGGAGTGGCTCTCCGAGAGAGAGAGAGCTTGGGGGCTTCA 421  
Db 174024 TGGACACACCATGAGGGGAGTGGCTCTCCGAGAGAGAGAGAGAGCTTGGGGGCTTCA 173965  
Qy 422 ACATTCAGGCTCTGAGGGATATGCTGCTCGAGAGAGAGAGAGAGAGCTTGGGGCTG 481  
Db 173964 ACATTCAGGCTCTGAGGGATATGCTGCTCGAGAGAGAGAGAGAGAGCTTGGGGCTG 173905  
Qy 482 GGCACCTCGAGTGAAGGCTGTGCTTCAGCAATTCAGCTTGTGCTGAGTCTCAAC 541  
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Qy 542 CCAAGGCTTGAAGGGGCTGCTTCACTGCTGAGAGAGG-GTNTATTCATGCAACCTTCCA 600  
Db 173844 CCAAGGCTTGAAGGGGCTGCTTCACTGCTGAGAGAGGATATTCATTCATTCCTCTG 173785  
Qy 601 TNC 604  
Db 173784 TNC 173781

RESULT 4  
AF61350 1380 bp mRNA linear ROD 21-DEC-2001  
LOCUS Mus musculus voltage-dependent calcium channel gamma-8 subunit  
DEFINITION (Ca<sub>v</sub>8) mRNA, complete cds.  
ACCESSION AF61350  
VERSION AF61350.1 GI:17974533  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 1380)  
AUTHORS Chu, P.-J., Robertson, H. M. and Beest, P. M.  
TITLE Calcium channel gamma subunits provide insights into the evolution  
of this gene family  
JOURNAL Gene 280 (1-2), 37-48 (2001)  
MEDLINE 1173816  
PUBMED 1173816  
REFERENCE 2 (bases 1 to 1380)  
AUTHORS Chu, P.-J., Robertson, H. and Beest, P. M.  
TITLE Direct Submision  
JOURNAL Submitted (14-MAR-2001) Department of Molecular and Integrative  
Physiology, University of Illinois, 407 S. Goodwin Ave., Urbana, IL  
61801, USA

FEATURES  
source  
1. .1380  
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GTLAVNIYIEREREAHCOSRDLAAGAGAGSGSGSPAILIRLSYRRYRRSRSS  
SNGSSBASPSRDSFQGPBPASTDLSMTYLSDPSPGSAVAAGLASAGGSGAGV  
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ORIGIN  
Query Match 59.1%; Score 387.4; DB 10; Length 1380;  
Best Local Similarity 99.7%; Pred. No. 66-81;  
Matches 388; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 69 TGAAGCCCCCGAGCTTCTGCTGTGCTGATCCCGGAGCGCGGAGCGCGGCT 128  
Db 1 TGAAGCCCCCGAGCTTCTGCTGTGCTGATCCCGGAGCGCGGAGCGCGGCT 60  
Qy 129 CCGCTGCCCCGGGTGTGAGCCACGCGCCCCCGGTTGCGAGTGAAGTGAAGTGA 188  
Db 61 CCGCTGCCCCGGGTGTGAGCCACGCGCCCCCGGTTGCGAGTGAAGTGAAGTGA 120  
Qy 189 AAAAGCTGAATGAAGAGAGGGGTTGTGTGTGAAGAGGGGTTAGGTACTACTGACC 248  
Db 121 AAAAGCTGAATGAAGAGAGGGGTTGTGTGTGAAGAGGGGTTAGGTACTACTGACC 180  
Qy 249 ACCATGCGGCGCTTGTGCGGCTTGTGCGCTCATGACCATGCGCATGCACTGACTG 308  
Db 181 ACCATGCGGCGCTTGTGCGGCTTGTGCGCTCATGACCATGCGCATGCACTGACTG 240  
Qy 309 CTCTACACAAGAGCTTCTCATCTGCAACACCAACCTTCAAGAGAGTATGACGAGCA 368  
Db 241 CTCTACACAAGAGCTTCTCATCTGCAACACCAACCTTCAAGAGAGTATGACGAGCA 300  
Qy 369 CCCCATGTGGGGGAGTGGCTCTCTCGAAGAGAGAGACCTTGGGGGCTTCAACATTCA 428  
Db 301 CCCCATGTGGGGGAGTGGCTCTCTCGAAGAGAGAGACCTTGGGGGCTTCAACATTCA 360  
Qy 429 GGCCTCTGGCGGATATGCTGCTGGAAG 457  
Db 361 GGCCTCTGGCGGATATGCTGCTGGAAG 389

RESULT 5  
AC008440 169997 bp DNA linear PRI 13-JUL-2002  
LOCUS Homo sapiens chromosome 19 clone CTC-33H23, complete sequence.  
DEFINITION AC008440  
ACCESSION AC008440  
VERSION AC008440.9 GI:21743728  
KEYWORDS HTG.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 16997)  
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.  
TITLE DOE Joint Genome Institute and Stanford Human Genome Center.  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 16997)  
AUTHORS DOE Joint Genome Institute.  
TITLE Direct Submision  
JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint  
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
3 (bases 1 to 16997)  
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.  
TITLE Direct Submision  
JOURNAL Submitted (01-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell  
Drive, Walnut Creek, CA 94598, USA  
4 (bases 1 to 16997)  
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.  
TITLE Direct Submision  
JOURNAL Submitted (13-JUL-2002) DOE Joint Genome Institute, 2800 Mitchell  
Drive, Walnut Creek, CA 94598, USA  
COMMENT On Jul 13, 2002 this sequence version replaced gi:1427251.

Draft Sequence Produced by DOE Joint Genome Institute  
www.jgi.doe.gov  
Finishing Completed at Stanford Human Genome Center  
www.shgc.stanford.edu  
Quality: Phrap Quality >=40 99.9% of Sequence;  
Estimated Total Number of Errors is 0.3.  
STS Content:  
WI-17997 G23480

NOTE: 90954 Ambiguous base. Probably T.

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## ORIGIN

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Best Local Similarity 81.2%; Pred. No. 9,9e-60;  
Matches 384; Conservative 0; Mismatches 82; Indels 7; Gaps 3;

QY 9 CACTGTGACCTCTTCCCTCTGTGAGCCACTGCTGCGCCGCCGCCGCCCTCTGTGAGCC 67  
DB 107335 CTTTACCCCTCTCCCGCGGAGGCTCTCTCTCCGCCGCCGCCCTCTCCAGCCCGCGG 107394  
QY 68 TTGAGGCCCCCAGGCTTCTGCTGCTGTGAT---CCCCAGCCGCGCGAGCCGCC 124  
DB 107395 CCCCCGCCCCCGGCTTCTGCTGCTGTGATGAGCCGCCGCCGCCGCCGCCGCC 107454  
QY 125 GCTTCCTGCTGCCCCGCTGTGAGCCAGCGCCCCCGGCTTGCAGTGTGAACTGAGTGC 184  
DB 107455 GCGCCCGCTGCCCCGCTGTGAGCCAGCGCCCCCGGCTGCTGCTGCTGCTGCTGCT 107514  
QY 155 ATTGAAGCGCTGGAATGAAGAGAGGGGTTTGTGCTGTAAGAGGGGCTTCAAGTCTACT 244  
DB 107515 GCTGAAGCGCTGGAAGAGAGAGGGGCTTGTGCTGTAAGAGGGGCTTCAAGTCTACT 107574  
QY 245 GACCAACATCGGCGCTTCTGCGGCTTGTGCTGTAAGAGAGGCTTCAAGTCTACT 304  
DB 107575 GACCAACATCGGCGCTTCTGCGGCTTGTGCTGTAAGAGAGGCTTCAAGTCTACT 107634  
QY 305 CTGGCTCTACAGAGAGCTTCTGTAAGAGAGAGGCTTCAAGTCTACT 361  
DB 107635 CTGGCTCTACAGAGAGCTTCTGTAAGAGAGAGGCTTCAAGTCTACT 107694  
QY 352 CGGACACCGGCTTCTGCGGCTTGTGCTGTAAGAGAGAGGCTTCAAGTCTACT 421  
DB 107695 CGGACACCGGCTTCTGCGGCTTGTGCTGTAAGAGAGAGGCTTCAAGTCTACT 107754  
QY 422 ACATTCAAGGCTTCTGCGGCTTGTGCTGTAAGAGAGAGGCTTCAAGTCTACT 474  
DB 107755 GCACCTGCGGCTTCTGAGAGATCTGCTGCTGTAAGAGAGGCTTCAAGTCTACT 107807

RESULT 6  
AF361346 1266 bp mRNA linear ROD 21-DEC-2001  
LOCUS AF361346  
DEFINITION Rattus norvegicus voltage-dependent calcium channel gamma-8 subunit  
(Ca<sub>v</sub>2g8) mRNA, complete cds.  
ACCESSION AF361346  
VERSION AF361346.1 GI:17974525  
KEYWORDS  
SOURCE  
ORGANISM  
Rattus norvegicus (Norway rat)  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
REFERENCE  
AUTHORS 1 (bases 1 to 1266)  
TITLE Chu, P.-J., Robertson, H.M. and Best, P.M.  
JOURNAL Of this gene family  
Gene 280 (1-2), 37-48 (2001)

MEDLINE 21601102  
PubMed 11738816  
REFERENCE 2 (bases 1 to 1266)  
AUTHORS Chu, P.-J., Robertson, H. and Best, P.M.  
TITLE Direct Submission  
JOURNAL Submitted (14-MAR-2001) Department of Molecular and Integrative  
Physiology, University of Illinois, 407 S. Goodwin Ave., Urbana, IL  
61801, USA

FEATURES  
source  
1.1266  
location/Qualifiers  
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CDS

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GVLAIVTYIERSREAHOSRDLKAGGAGSGSGSPATILRPSYFRYRRSRSS  
SRGSSSESPSRDASPGCPGPGFSTSTISMTLSRDSKSVAAGLASAGCGGAGV  
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## ORIGIN

Query Match 41.1%; Score 269.8; DB 10; Length 1266;  
Best Local Similarity 97.5%; Pred. No. 3.7e-53;  
Matches 274; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 177 CTGAGTCATTTGAACGCTGGAATGAAGAGAGGGGTTGTGCTGAAAGGGGCTTCAG 236  
DB 1 CTGAGTCATTTGAACGCTGGAATGAAGAGAGGGGTTGTGCTGAAAGGGGCTTCAG 60  
QY 237 GTACTACTGACCAACCATCGGCGCTTGGCGGCTTGTGCTGATGACCATGCGCATACG 296  
DB 61 GTACTACTGACCAACCATCGGCGCTTGTGCTGATGACCATGCGCATACG 120  
QY 297 ACTGACTACTGCTCTACAGAGAGCTCTACTGCAACACCAACCTCAGAGAGGT 356  
DB 121 ACTGACTACTGCTCTACAGAGAGCTCTACTGCAACACCAACCTCAGAGAGGT 180  
QY 357 GATGACGAGACCCCAATCGTGGGGGAGTGGCTCTCCGAGAAAGAGACCTTGGGGGC 416  
DB 181 GATGATGAGACCAACCAATCGTGGGGGAGTGGCTCTCCGAGAAAGAGACCTTGGGGGC 240  
QY 417 CTCACACATTAGGCTCTGCGGATATGCTGCTCGAAG 457  
DB 241 CTCACACATTAGGCTCTGCGGATATGCTGCTCGAAG 281

RESULT 7  
AC022318 190210 bp DNA linear HTG 31-AUG-2001  
LOCUS AC022318  
DEFINITION Homo sapiens chromosome 19 clone RP11-158G19, WORKING DRAFT  
SEQUENCE, 16 unordered pieces.  
ACCESSION AC022318.5 GI:15321555  
VERSION AC022318.5  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
SOURCE  
ORGANISM  
Homo sapiens  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE  
AUTHORS 1 (bases 1 to 190210)  
TITLE The sequence of Homo sapiens clone

us-10-060-066-2.rge

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Local Similarity 79.08; Pred. No. 3.9e-45;
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73 GCCCCCAGCTTGTGCTGTGTGATCCCCAGCCGCGCGACAGGCCCTCCGCTCCG 132
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133 TGCCCCGTGTGTGGCCCAAGGCCCCCCGGTTCAGTGTGAACCTGGAGTCATTGAAC 192
145891 TGCCCCGAGATGATGCCACAGCCCCCGGCTGCCGTGTCAACTGGAATGCTGAAGC 145950

193 GCTGGAATGAAGAAGAGGGGTTTGTGTGTGAAGAGGCGCTTACGAGTACTAGACCA 252
145951 GCTGGAAAGAAAGACGGGGGCTCTGGTGGAGAAAGGGGTGAGAGTCTCTGTGAAGAGG 146011

253 TGGCGGCTTTGCGGGCTTTTGGCTTCATGACCAATGGCACTGACCTAGTGGCTCT 312
146011 TGAACGCGCTTTCGCGCTCATGACATGGCCATCAGCACTGACTACTGGGCTCT 146068

313 ACACAAAGCTCTCATCTGTGAACACACCAA--CTCCACAGAGGTATGAGGAGCAACC 370
146069 ACAGCGCGGCTCTATCTGTGAACACCAACCACTCACAGCGCGCGCGAGCGAGGCC 146120

371 CCATCTGTGGGGGAGTGGCTCTCTCCAGAAAGAGACCTGTGGGGGCTCACACATTACG 430
146129 CCACCTGGGGGGGCGCGCGCGCTCTCGAGAAAGAGACCCCGCGGCTCTACGACTCGGG 146188

431 CCTTGGCGGATATGCTGCTCGTGAAGATGAGGTGACGAGAGGCC 474
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RESULT 8	AF361354	1366 bp	mRNA	linear	PRI 21-DEC-2001
LOCUS	AF361354				
DEFINITION	Homo sapiens voltage-dependent calcium channel gamma-8 subunit				
ACCESSION	AF361354				
VERSION	AF361354.1	GI:17974541			
					(CACNG8) mRNA, complete cds.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 1386)

AUTHORS Chu, P.-J., Robertson, H.M. and Best, P.M.

TITLE Calcium channel gamma subunits provide insights into the evolution of this gene family

JOURNAL Gene 280 (1-2), 37-48 (2001)

MEDLINE 21601102

PUBMED 11738816

REFERENCE 2 (bases 1 to 1386)

AUTHORS Chu, P.-J., Robertson, H. and Best, P.M.

TITLE Direct Submission

JOURNAL Submitted (14-MAR-2001) Department of Molecular and Integrative Physiology, University of Illinois, 407 S. Goodwin Ave., Urbana, IL 61801, USA

FEATURES

source Location/Qualifiers

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ORIGIN

Query Match 35.4%; Score 232.2; DB 9; Length 1386;

Best Local Similarity 78.3%; Pred. No. 2.8e-44;

Matches 306; Conservative 0; Mismatches 78; Indels 7; Gaps 2;

QY 73 GGGCCCGAGCTTCTGCTGTGTGATCCCCCAGCGCGGCGACGCGCCCTCCGC 132

DB 3 GGCACCCCGCTTCTGCTGTGCTTAAACCCCCCAAGCCGCGACGCGCCCGCGC 62

QY 133 TGCCCCGAGTGTGCCACGCGCCCGGTTGCCAGTGTGAACCTGAGTATTGAAC 192

DB 63 TGCCCCGAGTGTG-CGACGCGCCCGCGCTCCGTGTCAAATGAGTGTGCGTAAAGC 121

QY 193 GCTGGAATGAGAGAGGGGTTGTGTGTGAAGAGGCGTTGAGGTACTGACCA 252

DB 122 GCTGGAACGAAAGCGGGGCTCTGTGTGGAAGAGGGGTGCAAGTGTGTCGACGAGG 181

QY 253 TGGGGCGCTTGGCGCTTTTGGCTCAGACATGACCTGACCTGACTCTGGCTCT 312

DB 182 TGGGGCGCTTGGCGCTTGGCTCAGACATGACCTGACCTGACTCTGACTCT 241

QY 313 ACACAAGAGCTCTATCTGCAACACCAACCTCAGACAGAGTATGACG-----GAC 366

DB 242 ACAACGCGCGCTCTATCTGCAACACCAACCTCAGCGCGCGCGCAACGAGAACCC 301

QY 367 CACCCATGTGTGGGCGAGTGTGCTCTTCGAGAGAGAGACCTGAGGCGCTCAGACATT 426

DB 302 CTCACACTGTGGGCGAGTGTGCTCTTCGAGAGAGAGACCTGAGGCGCTCAGACACT 361

QY 427 CAGGCTCTGGGCGAGTATGCTGCTGAGAGG 457

DB 362 CGGCGCTCTGGAGAGTGTGCTGCTGAGAGG 392

RESULT 9

LOCUS AF234892

DEFINITION Homo sapiens putative voltage gated calcium channel gamma-8 subunit

ACCESSION AF234892

VERSION AF234892.1

KEYWORDS AF234892.1 GI:13182981

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 633)

AUTHORS Black, J.L., Ili, Kiyzer, T.J. and Lennon, V.A.

TITLE Proposed Homo sapiens voltage-gated calcium channel gamma-6 subunit

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 633)

AUTHORS Black, J.L., Ili, Kiyzer, T.J. and Lennon, V.A.

TITLE Direct Submission

JOURNAL Submitted (15-FEB-2000) Department of Psychiatry and Psychology, Mayo Clinic, 200 SW 1st Street, Rochester, MN 55905, USA

FEATURES

source Location/Qualifiers

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ORIGIN

Query Match 29.1%; Score 191.2; DB 9; Length 633;

Best Local Similarity 82.0%; Pred. No. 1.3e-34;

Matches 233; Conservative 0; Mismatches 48; Indels 3; Gaps 1;

QY 177 CTGAGTCAATTGAAACGCTGGAATGAAGAGGGGTTGTGTGTAAGAGGCGCTTCAG 236

DB 22 CAGGTGTGCTGAAGCGCTGGAACGAAGAGCGGGGCTCTGTGTCAAGAAAGGGGTGCAG 81

QY 237 GTACTACGACACATCGGGGCTTGGCGCTTTGGCCATGACCATGCGCATCAGC 296

DB 82 GTGCTGTGACGAGGTGTGGGCGCTTGGCGCTTGGCCATGACCATGCGCATCAGC 141

QY 297 ACTGACTAGTGGCTCTACACAAGAGCTCTCATCTGCAACACCAACCTCAGACG---A 353

DB 142 ACTGACTAGTGGCTCTACACGCGCGCTCATCTGCAACACCAACCTCAGCGCGCGC 201

QY 354 GGTATGACGAGACACCCCATGTGGGGGAGTGTGCTCTCCGAGAAAGAGACCTTGGG 413

DB 202 GGCACGACGAGAACCCCAACCGCGGGGCGCGCGCTCTCGAGAAAGAGACCCCGCGC 261

QY 414 GGCCTCACACTTGAAGGCTTGGCGGATATGCTGCTCTGAGAGG 457

DB 262 GGCTCACGACCTGAGGCTCTGAGAGATGTGCTGCTGAGAGG 305

RESULT 10

LOCUS AF288388

DEFINITION Homo sapiens calcium channel gamma subunit 8 (CACNG8) mRNA, partial cds.

AF288388 1281 bp mRNA linear PRI 16-MAR-2001

ACCESSION AF288388  
VERSION AF288388.1 GI:13357179  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Burgess, D.L., Gefrides, L.A., Foreman, P.J. and Noebels, J.L.  
TITLE A cluster of three novel Ca<sup>2+</sup> channel gamma subunit genes on chromosome 19q13.4: evolution and expression profile of the gamma subunit gene family  
JOURNAL Genomics 71 (3), 339-350 (2001)  
MEDLINE 21100909  
PUBMED 11170751  
REFERENCE  
AUTHORS Burgess, D.L., Gefrides, L.A., Foreman, P.J. and Noebels, J.L.  
TITLE Direct Submission  
JOURNAL Submitted (20-JUL-2000) Neurology, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
FEATURES  
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QY 210 GGTGTGTGTAAGGCGCTTCACTACTAGCAACCATCGCGCGCTTGGCGGT 269  
DB 1 GGCTCTGGTGCAGAAAGGGGTGCAAGTGTCTCTACACGGTGGCGCTTGGCGGC 60  
QY 270 TTGGGCTATGACATCGCATCAGCACTAGTACTGCTCTACACAAAGCTCTCATC 329  
DB 61 TTGGGCTATGACATCGCATCAGCACTAGTACTGCTCTACACGGCGCTCTCATC 120  
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DB 121 TGTCAACACCACTCAGCAGCAGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAG 180  
QY 387 GGCTCTCGAG 446  
DB 181 GGCGCTCGAG 240  
QY 447 TGCCTGGAAGG 457  
DB 241 TGCCTGGAAGG 251  
RESULT <1  
LOCUS AY037891 987 bp mRNA linear VRT 01-APR-2002

DEFINITION Gallus gallus calcium channel gamma 4 subunit (CACNG4) mRNA, complete cds.  
ACCESSION AY037891  
VERSION AY037891.1 GI:15418940  
KEYWORDS  
SOURCE  
ORGANISM Gallus gallus (chicken)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
REFERENCE  
AUTHORS Kious, B.M., Baker, C.V., Bromner-Fraser, M. and Knecht, A.K.  
TITLE Identification and characterization of a calcium channel gamma subunit expressed in differentiating neurons and myoblasts  
JOURNAL Dev. Biol. 243 (2), 249-259 (2002)  
MEDLINE 21881550  
PUBMED 11884034  
REFERENCE  
AUTHORS Kious, B.M., Bromner-Fraser, M. and Knecht, A.K.  
TITLE Direct Submission  
JOURNAL Submitted (04-JUN-2001) Biology, Caltech, Mail Code 139-74, Pasadena, CA 9125, USA  
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Best Local Similarity 65.9%; Pred. No. 3.7e-11;  
Matches 162; Conservative 0; Mismatches 60; Indels 24; Gaps 1;  
QY 214 TGTGTGTGTAAGGCGCTTCACTACTAGCAACCATCGCGCGCTTGGCGGT 273  
DB 5 TGTGTGTGTAAGGCGCTTCACTACTAGCAACCATCGCGCGCTTGGCGGT 64  
QY 274 GGCTCATGACATCGCATCAGCACTAGTACTGCTCTACACAAAGCTCTCATGCA 333  
DB 65 GGCTCATGACATCGCATCAGCACTAGTACTGCTCTACACAAAGCTCTCATGCA 124  
QY 334 AACACCACTCAGCAG 393  
DB 125 ACGGACCAACATCAG 163  
QY 394 CCGAG 453  
DB 164 ---CGAG 220  
QY 454 AAGGTA 459  
DB 221 AAGGTA 226  
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LOCUS HSCACNG1 720 bp DNA linear PRI 07-JAN-2000  
DEFINITION Homo sapiens calcium channel gamma 4 subunit (CACNG4) gene, exon 1.  
ACCESSION AF142622

VERSION AF142622.1 GI:6062998  
 KEYWORDS  
 SEGMENT 1 of 4  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE  
 AUTHORS Burgess, D.L., Davis, C.F., Gefridis, L.A. and Noebels, J.L.  
 TITLE Identification of three novel Ca(2+) channel gamma subunit genes  
 reveals molecular diversification by tandem and chromosome  
 duplication  
 JOURNAL Genome Res. 9 (12), 1204-1213 (1999)  
 MEDLINE 20082967  
 PUBMED 10613843  
 REFERENCE 2 (bases 1 to 720)  
 AUTHORS Burgess, D.L., Caley, D.F., Lisa, G.A. and Jeffrey, N.L.  
 TITLE Direct Substitution  
 JOURNAL Submitted (12-APR-1999) Neurology, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
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 Best Local Similarity 66.8%; Pred. No. 7.8e-10;  
 Matches 123; Conservative 0; Mismatches 61; Indels 0; Gaps 0;  
 QY 214 TGTGTTGTAAGGCGCTTACGATGCTAGTACGACCACTGCGCGCTTTG 273  
 DB 239 TCGATGCGACCGCGGCTGCGATGCTGCTGCAACGCGGAGCTTCGCGCTTCT 298  
 QY 274 GCGTATGACCATGCGCATGACGACGATGCTGCTACACAGAGCTTCATCTGCA 333  
 DB 299 CGCTATGCGCATGCGCATGCGACGACGATGCTGCTGCTGCAAGCGGACATCTGCA 358  
 QY 334 ACACCAACCACTTACGACGAGGTGATGACGACCAACCCCATGCTGCGGAGCTGCTCT 393  
 DB 359 ACGGACCACTGACGATGACGACGAGCGGCGCGCGCGCGCGCGGAGCTTCA 418  
 QY 394 CCGA 397  
 DB 419 CCGA 422  
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 ARI65149 984 bp DNA linear PAT 17-OCT-2001  
 LOCUS Sequence 1 from patent US 6274380.  
 DEFINITION ARI65149  
 ACCESSION ARI65149  
 VERSION ARI65149.1 GI:16238585  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 984)  
 AUTHORS Duckworth, D.M., Malcom, and Hayes, P.D.  
 TITLE Catecholamines polymorphisms and expression systems  
 JOURNAL Patent: US 6274380-A 1 14-AUG-2001;  
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 QY 274 GCGTATGCGCATGCGCATGCGACGACGATGCTGCTTACACAGAGCTTCATCTGCA 333  
 DB 65 CGCTATGCGCATGCGCATGCGACGACGATGCTGCTTACACAGAGCTTCATCTGCA 124  
 QY 334 ACACCAACCACTTACGACGAGGTGATGACGACCAACCCCATGCTGCGGAGCTGCTCT 393  
 DB 125 ACGGACCACTGACGATGACGACGAGCGGCGCGCGCGCGCGGAGCTTCA 184  
 QY 394 CCGA 397  
 DB 185 CCGA 188  
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 AX101260 984 bp DNA linear PAT 10-APR-2001  
 LOCUS Sequence 1 from Patent WO0121791.  
 DEFINITION AX101260  
 ACCESSION AX101260  
 VERSION AX101260.1 GI:13620050  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1  
 AUTHORS Clare, J.J., Plumpton, M., Moss, F.J. and Saneau, P.  
 TITLE Stergazin-like neuronal ca2+-channel gamma subunit polypeptides  
 JOURNAL Patent: WO 0121791-A 1 29-MAR-2001;  
 GLAXO GROUP LIMITED (GB)  
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Db 185 CCCA 188

Search completed: May 22, 2004, 16:19:23  
Job time : 2053 secs

RESULT 15  
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LOCUS Mus musculus mRNA for calcium channel gamma 4 subunit (CACNG4)  
DEFINITION

gene).

ACCESSION AJ272045 GI:7452995

VERSION CACNG4 gene; calcium channel gamma 4 subunit.

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 Klugbauer, N., Dai, S., Specht, V., Lacinova, L., Marais, E., Bohn, G.

AUTHORS and Hofmann, F.

TITLE A family of gamma-like calcium channel subunits

JOURNAL FEBS Lett. 470 (2), 189-197 (2000)

MEDLINE 20200313

PUBMED 10734232

REFERENCE 2 (bases 1 to 984)

AUTHORS Klugbauer, N.

TITLE Direct Submission

JOURNAL Submitted (08-FEB-2000) Klugbauer N., Institut fuer Pharmakologie

und Toxikologie, Technische Universitaet Muenchen, Biedersteiner

Str. 29, 81827 Muenchen, GERMANY

Location/Qualifiers

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ORIGIN

Query Match 13.2%; Score 86.4; DB 10; Length 984;

Best Local Similarity 66.8%; Pred. No. 7.8e-10;

Matches 123; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 214 TGTGTTGTAAGGCGCTCAAGTACTGACACCATCGGCGCTTTG 273

DB 5 TCGATGCGACCGCGGCTGACATGCTGACACGCGGAGCTTGCGCGCTTC 64

QY 274 GCCTCATGACCATGCGCATGACGACTGAGCTCTACAGAGCTCATCTGCA 333

DB 65 CGCTCATGCGCATGCGCATGCGCATGAGCTGCTGCTGCTGCTGCTGCTGCA 124

QY 334 ACACCAACCACTCAGCAGAGTATGACGACCAACCCATCGTGGGCGAGTGGCTCT 393

DB 125 AGGCAACCACTGACATGAGAGCGGCGCGCGCGCGCGCTCGGCGACCTCA 184

QY 394 CCGA 397

DB 185 CCCA 188

